摄入不同食用油一周对大鼠尿蛋白质组的影响

苏妍[1]，高友鹤[1*]

（1. 北京师范大学 生命科学学院 基因工程药物及生物技术北京市重点实验室 北京 100875）

摘要：

目的：通过分析大鼠摄入橄榄油、黄油、猪油、氢化植物油、菜籽油一周后尿液蛋白质组及翻译后修饰的变化，探究不同食用油对大鼠机体的影响。

方法：设置六组 Wistar 雄性大鼠平行实验，A 组作为对照，B-F 组分别摄入不同食用油，收集一周后的尿液样品，通过高效液相色谱串联质谱联用（LC-MS/MS）的非标记定量蛋白质组学技术进行鉴定。筛选尿液蛋白质组的差异蛋白及差异翻译后修饰进行功能分析。

结果：摄入不同种类食用油后大鼠均产生了大量与代谢相关的蛋白质及生物学通路，但不同组别共有的差异蛋白较少。此外，橄榄油组和黄油组富集到了很多与神经系统相关的生物学通路，菜籽油组产生了较多与免疫相关的差异蛋白和生物学通路。

结论：大鼠摄入食用油一周后尿液蛋白质组展现出显著的变化，且各类食用油给大鼠尿蛋白质组带来的影响彼此间存在差异，这种影响在大鼠机体层面上是全方位、多维度的。蛋白质组的翻译后修饰所发生的变化较小。

关键词：尿液蛋白质组；食用油；翻译后修饰

The Effect of Ingesting Different Edible Oils for One Week on the Urinary Proteome of Rats

Yan Su[1], Youhe Gao[1*]

(1. Gene Engineering Drug and Biotechnology Beijing Key Laboratory, College of Life Sciences， Beijing Normal University, Beijing 100875, China)

Abstract:

基金项目：中国国家重点研发计划（2023YFA1801900），北京自然科学基金（L246002），北京师范大学（11100704）

作者简介：1.苏妍（2002.1—），女，硕士研究生，主要研究方向：尿液生物标志物。

通信联系人：高友鹤（1964.06—），男，教授，博士生导师，主要研究方向：尿液蛋白质组学与尿液生物标志物。E-mail: gaoyouhe@bnu.edu.cn.

Objective: To explore the impacts of different edible oils on the rat body by analyzing the changes in the urinary proteome and post-translational modifications after rats were fed with olive oil, butter, lard, hydrogenated vegetable oil, and rapeseed oil for one week.

Methods: Six groups of parallel experiments were set up using Wistar male rats. Group A served as the control group, while groups B - F were fed with different edible oils respectively. Urine samples were collected one week later and identified by the label-free quantitative proteomics technique of high-performance liquid chromatography-tandem mass spectrometry (LC-MS/MS). The differential proteins in the urinary proteome and the differential post-translational modifications were screened for functional analysis.

Results: After rats ingested different kinds of edible oils, a large number of metabolism-related proteins and biological pathways were generated in all rats. However, there were relatively few differential proteins shared among different groups. In addition, the olive oil group and the butter group were enriched with many biological pathways related to the nervous system, while the rapeseed oil group produced more differential proteins and biological pathways related to immunity.

Conclusions: The urinary proteome of rats showed significant changes after being fed with edible oils for one week. Moreover, the impacts of various edible oils on the urinary proteome of rats were different from each other, and these impacts were comprehensive and multi-faceted at the level of the rat body. The changes in the post-translational modifications of the proteome were relatively minor.

Key words: Urinary proteome; Edible Oil; Post-translational modification

1　前言

食用油作为日常饮食中的重要组成部分，在全球范围内被广泛食用，为人体提供了必需的脂肪酸和能量，对维持人体正常生理功能起着关键作用[1]。随着人们对健康关注度的不断提高，不同食用油的营养价值和潜在健康影响逐渐成为研究热点。

既往研究表明，不同种类的食用油因其独特的脂肪酸组成和营养成分，具有不同的生理功能和健康效应[2]。例如，橄榄油是地中海饮食的主要脂肪来源，富含单不饱和脂肪酸，被认为具有降低心血管疾病风险等有益作用[3]；黄油含有较多的饱和脂肪酸，过量摄入可能与心血管疾病风险增加相关[4]；猪油是亚洲地区人群食用较多的动物油，其脂肪酸组成较为均衡，包括 52.1% 饱和脂肪酸、35.8% 单不饱和脂肪酸和 11.6% 多不饱和脂肪酸，对健康的影响存在争议[5][6]；氢化植物油因含有反式脂肪酸，可能对心血管健康产生不良影响[7]；菜

籽油作为一种植物油，具有相对平衡的脂肪酸比例，且抗氧化剂等营养成分[8]。

鉴于不同食用油在脂肪酸组成和营养特性上的显著差异，以及它们在日常饮食中的普遍食用情况，本研究选择橄榄油、黄油、猪油、氢化植物油和菜籽油这几种具有代表性的食用油进行研究。为避免大鼠短期生长发育对实验结果的干扰，我们选择进行不同实验组和对照组的组间平行对照。通过对比大鼠尿蛋白质组的差异，我们初步探究了短期食用不同食用油对大鼠体内代谢过程可能存在的影响，为深入了解其对人体健康的潜在影响提供一定的理论参考和实验依据。

2　材料与方法

2.1 实验动物及模型建立

7 周龄 Wistar 雄性大鼠 30 只，体重约为 200g，购于北京维通利华实验动物生物技术有限公司。所有大鼠在标准环境中饲养（室温（22±1）℃，湿度 65%-70%）。将所有大鼠在新环境中饲养三天后开始实验，一切实验操作遵循北京师范大学生命科学学院伦理委员会的审查和批准，批准编号为 CLS-AWEC-B-2022-003。

本实验将对照组设为 A 组，不额外摄入食用油。其他组别分别摄入不同类型食用油，分别为橄榄油（B 组）、黄油（C 组）、猪油（D 组）、氢化植物油（E 组）、菜籽油（F 组），每组 5 只大鼠。根据《2015—2020 美国居民膳食指南》和《中国居民膳食指南》推荐分别计算出成人每天摄入食用油的量与体重的比值，再根据人和动物按体表面积折算的等效剂量比值表，大鼠服用剂量约为人的 6.25 倍，换算得到大鼠的每日的食用油摄入量，如表 1 所示。

表 1 大鼠的每日的食用油摄入量

	橄榄油	黄油	猪油	氢化植物油	菜籽油
成人食用油摄入量与体重的比值/((g/Kg)/天)	0.5	0.44	0.45	0.45	0.45
大鼠食用油摄入量/(g/天)	0.625	0.55	0.56	0.56	0.56

在适应性喂养结束后，于每日 17：00 给不同组别大鼠食用对应食用油，持续 7 天。第 7 天大鼠摄入食用油后，将大鼠分别放置在代谢笼中，让其在笼中代谢，过夜 12h 后收集尿液。最后将收集到的尿液样本 3000r/min 离心处理 30 min 后，放入−80℃冰箱保存。

2.2 尿液样品的处理

尿蛋白提取流程：先将尿样解冻，随后在 4℃环境下以 12000×g 的离心力离心 30 min，把上清液转移至新的 EP 管里。之后加入四倍体积的无水乙醇，混匀后放入 -20℃冰箱沉淀一天。第二天，将混合液在 12000×g、4℃条件下离心 30 min，倒掉上清，把蛋白沉淀重新悬浮于裂解液（含 8 mol/L 尿素，2 mol/L 硫脲，25 mmol/L 二硫苏糖醇，50 mmol/L）中，又在 12000×g、4℃条件下离心 30 min，保留上清液，最后用 Bradford 方法测定蛋白质的浓度。

蛋白酶解流程：取 100μg 尿蛋白样品放入 EP 管，加入 25 mmol/L NH_4HCO_3 溶液使总体积为 200μL 作为备用样本。接着往管中加入二硫苏糖醇溶液（Dithiothreitol，DTT，Sigma），直至其终浓度为 20mM，放入 95℃金属浴加热 10min 后冷却到室温，再加入碘乙酰胺（Iodoacetamide，IAA，Sigma）至浓度 50mM，常温避光静置 40 min。随后对 10 kDa 超滤管的滤膜（Pall，Port Washington，NY，USA）进行洗膜：首先加入 200μL UA 溶液（8 mol/L 尿素，0.1 mol/L Tris - HCl，pH 8.5），在 14000×g、18℃条件下离心 10 min，重复两次；把准备好的样本加入超滤管，在 14000×g、18℃条件下离心 40 min；接着加 200μL UA 溶液，在 14000×g、18℃条件下离心 30 min，重复两次；随后加入 25 mmol/L NH_4HCO_3 溶液，在 14000×g、18℃条件下离心 30 min，重复两次；最后按胰酶：蛋白为 1：50 的比例加入胰蛋白酶（Trypsin Gold，Promega，Fitchburg，WI，USA），在 37℃下孵育过夜。过夜后，离心收集酶解后的滤液，用 Oasis HLB 固相萃取柱除盐后真空干燥，得到肽段冻干，置于 -80℃保存。

2.3 LC-MS/MS 串联质谱分析

把肽段放置于 0.1% 甲酸水中进行复溶，通过这样的操作将肽段浓度调节至 0.5 μg/μL。随后，让肽段通过 Thermo ESAY-Nlc1200 液相系统来完成分离，该液相系统的参数设置情况如下：洗脱时间控制在 90 min，而洗脱梯度具体是由 A 相（0.1% 甲酸）以及 B 相（80% 乙腈）所构成。最后，使用 Orbitrap Fusion Lumos Tribird 质谱仪，针对分离后的肽段多次进行数据依赖质谱数据采集，且重复采集次数为三次，所采用的采集模式为数据非依赖型模式。

2.4 数据库搜索

使用 Spectronaut Pulsar（Biognosys AG, Switzerland）软件对质谱仪采集结果的 raw 文件

进行数据库检索，使用 SwissProt Human 数据库进行对比。通过将 MS2 中各自片段离子的峰面积相加，计算出肽的丰度。蛋白质强度由各自的肽丰度相加计算蛋白质丰度。

2.5 Open-pFind 非限定性修饰搜索

运用 pFind Studio 软件（版本 3.2.1，中国科学院计算技术研究所），针对每个样本所进行的 3 次技术重复展开非限定性修饰搜索操作，在搜索过程中采用默认的参数设置。所使用的数据库是从 UniProt 下载的 Rattus norvegicus 数据库，该数据库已更新至 2024 年 9 月。仪器类型设定为 HCD - FTMS，所选用的酶为胰蛋白酶，且具备酶全特异性，允许最多存在 2 个漏切位点。前体质量容差设定为 ±20 ppm，碎片质量容差同样设定为 ±20 ppm，同时选择开放搜索模式。而筛选条件明确规定，在肽水平上错误发现率（FDR）需小于 1%。

2.6 蛋白数据生物信息分析

每一个样品均进行 3 次技术重复，将获得的数据取平均值后用于统计学分析。本实验分别进行食用油组（B、C、D、E、F 组）与对照组（A 组）的成组比较，筛选差异蛋白，差异蛋白筛选条件为：组间变化倍数（FC, Fold change）≥ 1.5 或 ≤ 0.67，双尾配对 t 检验分析的 P 值 ＜ 0.05。筛选到的差异蛋白通过 Uniprot 网站（https://www.uniprot.org）查询名称及功能，通过 DAVID 数据库（https://david.ncifcrf.gov）进行生物学功能富集分析。并在 Pubmed 数据库（https://pubmed.ncbi.nlm.nih.gov）中检索已报道文献，从而对差异蛋白进行功能分析。

2.7 蛋白翻译后修饰生物信息分析

利用 Open-pFind 开展非限定性修饰搜索，获得每个样本的翻译后修饰 PROTEIN 文件。随后在 GitHub 平台（网址是 https://github.com/daheitu/scripts_for_pFind3_protocol.io）下载名为 pFind_protein_contrast_script 的 Python 脚本，运用该脚本来对不同样本的翻译后修饰鉴定结果（即 PROTEIN 文件）进行汇总操作。同样分别进行食用油组（B、C、D、E、F 组）与对照组（A 组）的成组比较，筛选差异修饰。差异修饰筛选条件为： FC ≥ 1.5 或 ≤ 0.67，双尾配对 t 检验分析的 P 值 ＜ 0.05。对筛选到的差异修饰所在的蛋白通过 Uniprot 网站（https://www.uniprot.org）查询名称及功能。

3　结果与讨论

3.1 大鼠行为学观察

在实验开始前、实验结束后分别称量大鼠体重（图 1a），对比发现实验组大鼠除 E 组外体重增加量均高于对照组。统计大鼠实验过程中的进食量（图 1b），对比发现实验组大鼠进食量均高于对照组。观察大鼠对食用油的喜好程度，发现 C、D 组大鼠摄入黄油、猪油更快速，而 E 组大鼠对所摄入的氢化植物油明显排斥。此外，E 组大鼠在实验过程中逐渐出现口周毛发脱落现象，推测可能原因是：氢化植物油为固态油，实验喂食前会先融化该油随后给大鼠喂食，由于大鼠排斥氢化植物油，喂食后大鼠将其吐出导致在口周凝固结块，随后在清理过程中将口周毛发一同扯下。

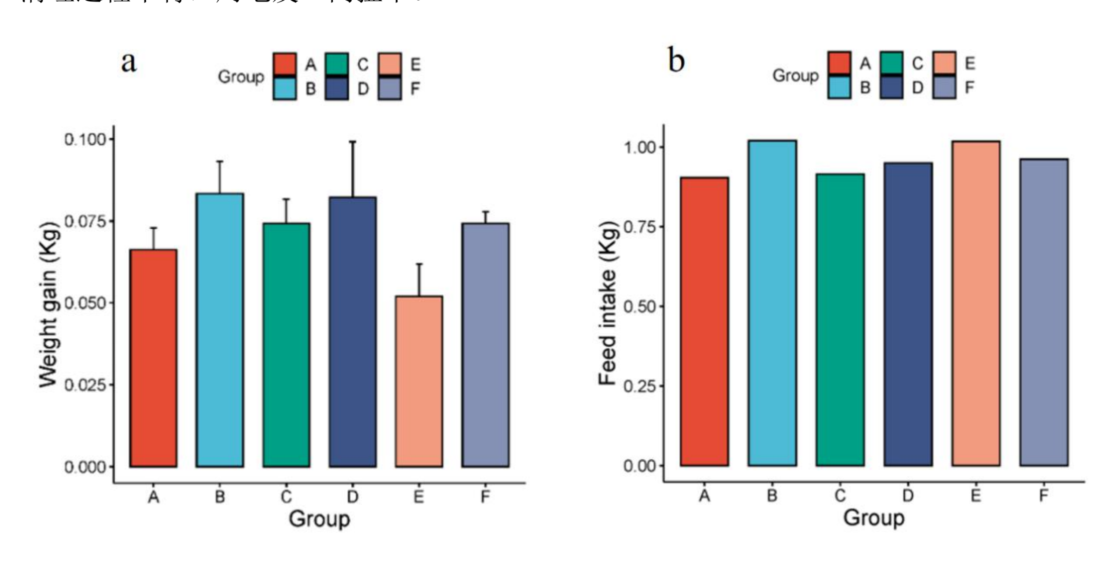


图 1　a. 喂油前后大鼠体重增加量; b. 喂油期间大鼠进食量.

3.2 尿液蛋白质组成组分析

3.2.1 随机分组

将对照组样品（n=5）和实验组样品（n=5）随机分成两组，共有 126 种分组。在所有随机组合类型中，按照相同的筛选条件计算所有随机次数的差异蛋白平均数。差异蛋白平均数与正常分组下得到的差异蛋白的比值即为随机产生的差异蛋白比例，列于表 2。 这些结果表明，随机生成的差异蛋白均较少，筛选差异蛋白的可信度较高。说明我们得到的差异蛋白大部分不是随机产生的，而是由于短期摄入不同食用油造成的影响。

表 2 随机分组得到的随机产生差异蛋白比例

对照组-实验组	A-B	A-C	A-D	A-E	A-F

随机产生蛋白比例	5.6%	6.6%	6.4%	12.7%	5.5%

3.2.2 橄榄油组尿液蛋白质组成组分析

3.2.2.1 差异蛋白

将橄榄油组（B 组）与对照组（A 组）尿液蛋白质进行比较，筛选差异蛋白条件为：变化倍数 FC ≥ 1.5 或 ≤ 0.67，双尾配对 t 检验 $P < 0.05$。结果表明，相对于对照组，橄榄油组共鉴定到 94 个差异蛋白，其中 17 种下调，77 种上调。将差异蛋白按 FC 由小到大的顺序排列，通过 Uniprot 进行检索，详细信息列于表 3。

表 3 橄榄油组与对照组以 FC≥1.5 或≤0.67，P<0.05 筛选的尿蛋白质组差异蛋白

Uniprot ID	Protein name	Fold change	P-value	Trend
F1LMP1	Alpha-1,3-mannosyl-glycoprotein 4-beta-N-acetylglucosaminyltransferase A	0.000	3.81E-02	↓
Q5XIF6	Tubulin alpha-4A chain	0.020	3.84E-02	↓
P18614	Integrin alpha-1	0.047	2.81E-02	↓
F1LW74	IQ motif containing GTPase activating protein 2	0.094	2.22E-02	↓
A0A0G2K0V8	Nuclear distribution C, dynein complex regulator	0.104	2.73E-02	↓
M0R7T1	Phosphatase and actin regulator 4	0.180	2.94E-02	↓
A0A0G2JSZ2	Seminal vesicle secretory protein 4	0.195	4.87E-02	↓
P25236	Selenoprotein P	0.213	1.71E-03	↓
F1LQM1	Alpha-2u-globulin	0.267	4.55E-02	↓
Q8R2H2	Integrin beta-3	0.269	4.35E-03	↓
P34058	Heat shock protein HSP 90-beta	0.318	8.62E-03	↓
B1WBS5	Sodium/mannose cotransporter SLC5A10	0.349	4.09E-02	↓
Q9JJI3	Major urinary protein 4	0.386	3.35E-02	↓
P16573	Carcinoembryonic antigen-related cell adhesion molecule 1	0.398	2.46E-02	↓
F8WG88	Follistatin-related protein 1	0.404	4.87E-02	↓
A0A0G2JXZ9	protein-tyrosine-phosphatase	0.412	7.16E-03	↓
G3V9J1	Murinoglobulin 2	0.467	4.89E-02	↓
A0A0G2JTX6	C-type lectin domain containing 5A	1.574	3.76E-02	↑

M0R7Q2	Ig-like domain-containing protein	1.645	4.40E-02	↑
Q5U2Q3	Ester hydrolase C11orf54 homolog	1.835	1.96E-02	↑
Q9ESS6	Basal cell adhesion molecule	1.840	3.93E-02	↑
F1M663	Ig-like domain-containing protein	2.041	3.09E-03	↑
P70490	Lactadherin	2.055	4.93E-02	↑
P04785	Protein disulfide-isomerase	2.093	3.12E-02	↑
A0A0G2JXT8	Filamin B	2.100	4.10E-02	↑
P07150	Annexin A1	2.313	3.33E-02	↑
D3ZQP6	Semaphorin 7A	2.331	2.94E-02	↑
F7F3I7	Semaphorin 4A	2.381	4.06E-02	↑
Q5U2V4	Phospholipase B-like 1	2.407	2.97E-02	↑
A0A0G2JZN1	deleted	2.460	2.72E-02	↑
Q5BK81	Prostaglandin reductase 2	2.481	6.86E-03	↑
F1LSV0	Semaphorin 4B	2.523	1.37E-02	↑
F1LPC6	Carboxypeptidase D	2.532	9.34E-03	↑
D3ZHA1	Beta-1,4-glucuronyltransferase 1	2.608	4.44E-02	↑
D4ABU7	Triggering receptor expressed on myeloid cells 1	2.614	4.02E-02	↑
A0A140TAI2	Biotinidase	2.642	1.83E-02	↑
A0A0G2JY48	receptor protein-tyrosine kinase	2.778	3.02E-04	↑
M0RDL2	deleted	2.869	2.35E-02	↑
P09034	Argininosuccinate synthase	2.873	4.08E-02	↑
G3V647	Pyridoxal kinase	2.958	3.32E-02	↑
P15429	Beta-enolase	2.983	3.95E-02	↑
B1WBN7	FAM20C	2.996	3.27E-02	↑
Q6AYE5	Out at first protein homolog	3.081	1.77E-02	↑
Q00657	Chondroitin sulfate proteoglycan 4	3.180	1.19E-02	↑
Q66HG4	Galactose mutarotase	3.231	2.82E-02	↑
P80254	D-dopachrome decarboxylase	3.465	4.00E-02	↑
D3ZBS2	Inter-alpha-trypsin inhibitor heavy chain H3	3.466	4.06E-02	↑

B5DEI2	Amine oxidase	3.502	3.78E-02	↑
Q6P7S1	Acid ceramidase	3.578	1.69E-02	↑
Q80ZA3	Serine	3.626	1.73E-02	↑
M0RAM5	Glutathione peroxidase	3.773	2.25E-03	↑
Q66H12	Alpha-N-acetylgalactosaminidase	3.783	1.41E-02	↑
P04905	Glutathione S-transferase Mu 1	3.885	9.36E-03	↑
Q64361	Latexin	3.898	2.47E-02	↑
Q6JE36	Protein NDRG1	4.046	1.28E-02	↑
F1MAN8	Laminin subunit alpha 5	4.061	4.57E-02	↑
Q80WD1	Reticulon-4 receptor-like 2	4.067	2.21E-02	↑
B0BN46	Grhpr protein	4.087	3.79E-02	↑
Q9R1T3	Cathepsin Z	4.163	1.10E-02	↑
M0R3V4	Myeloid-derived growth factor	4.195	5.85E-03	↑
P19804	Nucleoside diphosphate kinase B	4.259	4.81E-02	↑
Q64573	Liver carboxylesterase 1F	4.302	4.58E-02	↑
B1H232	Immunoglobulin superfamily containing leucine-rich repeat	4.366	4.88E-03	↑
A0A0G2JZS9	Ig-like domain-containing protein	4.371	4.73E-02	↑
P47853	Biglycan	4.378	4.97E-02	↑
A2IBE0	Membrane-bound carbonic anhydrase 14	4.589	1.39E-03	↑
A0A0G2JXN4	Glutathione peroxidase	4.644	3.44E-02	↑
A0A0G2JV12	Collagen type XV alpha 1 chain	4.660	4.47E-02	↑
Q4FZV0	Beta-mannosidase	4.713	9.92E-04	↑
Q32KJ6	N-acetylgalactosamine-6-sulfatase	4.750	1.15E-02	↑
P22734	Catechol O-methyltransferase	4.764	9.59E-04	↑
O35760	Isopentenyl-diphosphate Delta-isomerase 1	4.936	4.64E-02	↑
Q675A5	Lysosomal phospholipase A and acyltransferase	5.090	2.79E-02	↑
Q99M75	Reticulon-4 receptor	5.202	1.61E-02	↑
Q920A6	Retinoid-inducible serine carboxypeptidase	5.230	1.80E-02	↑
F1LP42	Hedgehog protein	5.268	4.94E-03	↑

Q5PPH0	Enolase-phosphatase E1	5.578	2.77E-02	↑
Q641Z7	Cyclic GMP-AMP phosphodiesterase SMPDL3A	5.628	4.19E-02	↑
A0A0H2UHH2	Amyloid P component, serum	5.642	1.99E-02	↑
P45479	Palmitoyl-protein thioesterase 1	5.755	1.20E-02	↑
D4ACR1	RCG64219-like	6.063	4.08E-02	↑
Q9EQV6	Tripeptidyl-peptidase 1	6.607	2.50E-02	↑
F1M7B3	Ig-like domain-containing protein	6.880	1.68E-02	↑
Q562C9	Acireductone dioxygenase	7.269	2.55E-02	↑
G3V722	Beta-1,4-galactosyltransferase	7.724	4.13E-02	↑
G3V862	Angiopoietin-like 2	7.891	1.18E-02	↑
G3V7N8	Galectin 9	7.948	4.30E-03	↑
Q5I0D5	Phospholysine phosphohistidine inorganic pyrophosphate phosphatase	8.140	3.59E-02	↑
D3ZTV3	Leucine-rich repeat transmembrane protein FLRT2	8.891	5.15E-03	↑
F1M091	Kallikrein m	9.236	1.33E-02	↑
D3ZP44	SLIT and NTRK-like family, member 6	9.527	1.06E-02	↑
Q5FVH2	5'-3' exonuclease PLD3	9.588	7.19E-03	↑
P53369	Oxidized purine nucleoside triphosphate hydrolase	10.262	2.83E-03	↑
F1M0B7	deleted	11.606	4.74E-02	↑

3.2.2.2 差异蛋白功能分析

将鉴定到的差异蛋白于 Pubmed 数据库进行文献检索。

在差异蛋白中下调幅度最大、变化为“从有到无”的差异蛋白为 Alpha-1,3-mannosyl-glycoprotein 4-beta-N-acetylglucosaminyltransferase A (FC=0, P=3.81E-02)，研究表明 N - 乙酰氨基葡萄糖基转移酶 IV 负责将尿苷二磷酸 - N - 乙酰氨基葡萄糖转移到特定的糖蛋白结构上，参与肿瘤相关 N - 聚糖的糖基化修饰，这一过程可能与糖尿病的发病机制存在关联[9]。

此外，还有部分蛋白在已有文献研究中显示出其与橄榄油、氧化应激或代谢方面的相关性：

IQ motif containing GTPase activating protein 2 (FC=0.094, P= 2.22E-02)在调节肝脏燃料储存，特别是糖原水平方面具有重要的作用，在缺乏该蛋白的雌鼠中出现了糖原积累显著减少的现象[10]。

Selenoprotein P (FC=0.213, P=1.71E-03)作为主要的硒转运蛋白，在维持体内硒稳态和硒蛋白表达层次结构方面起着重要作用。充足的硒供应通过 SELENOP 对大脑的正常发育和功能至关重要，对男性生育能力、适当的神经功能和硒代谢至关重要[11]。

Heat shock protein HSP 90-beta (FC=0.318, P=8.62E-03)在心肌细胞中表达丰富，通过维持谷胱甘肽（一种主要的氧化还原介质）的水平，参与维持心血管系统的氧化还原稳态[12]。

Glutathione peroxidase (FC=3.773, P=2.25E-03)是一种重要的抗氧化酶，它在保护细胞免受氧化应激损伤中起着关键作用。研究中发现，橄榄油中的一种多酚类化合物 ligstroside 能够增加 Glutathione peroxidase 的表达，这可能有助于提高细胞的抗氧化能力，从而保护细胞免受氧化应激引起的损伤[13]。

Angiopoietin-like 2 (FC=7.891, P=1.18E-02)是一种重要的促血管生成因子，近年来也被发现参与介导炎症过程。其在多种炎症性疾病中表达上调，并与炎症相关信号通路的直接调控有关[14]。

Leucine-rich repeat transmembrane protein FLRT2 (FC=8.891, P= 5.15E-03)通过升高酰基辅酶 A 合成酶长链家族成员 4 的表达促进脂质过氧化，进而触发铁死亡，从而抑制人类膀胱癌细胞的恶性表型，被确定为一种肿瘤抑制基因[15]。

Oxidized purine nucleoside triphosphate hydrolase (FC=10.262, P= 2.83E-03)将氧化的嘌呤核苷三磷酸（如 8-oxo-dGTP 和 2-羟基-dATP）水解为单磷酸，从而防止这些氧化核苷酸在复制过程中的错误掺入[16]。

3.2.2.3 差异蛋白富集生物学过程分析

使用 DAVID 数据库对成组分析鉴定到的 94 个差异蛋白进行生物学过程（Biological process, BP）富集分析。结果显示，共有 29 个 BP 通路被显著富集（P<0.05），详细信息列于图 2。

在富集到的通路中有很多与神经系统相关的通路，包括轴突导向、神经嵴细胞迁移、参与轴突导向的轴突伸展的负调控、胼胝体发育、轴突发生、突触组装的正调节、神经元投射发育的负调节。多项研究表明特级初榨橄榄油具有重要的神经保护活性，这些作用与其特定的酚类成分密切相关，因此可能富集出神经系统相关通路[17][18][19]。

通路“调节内皮细胞迁移”在橄榄油研究中也被提到：羟基酪醇和 secoiridoids 都是橄榄油中的成分，它们在调节与内皮细胞增殖和迁移以及调节与心脏组织中心力衰竭相关的蛋白质中发挥作用[20]。

此外，脂质储存的负调节、脂质分解代谢过程、脂质生物合成过程的负调控，这 3 条通路与脂肪的摄入直接相关。

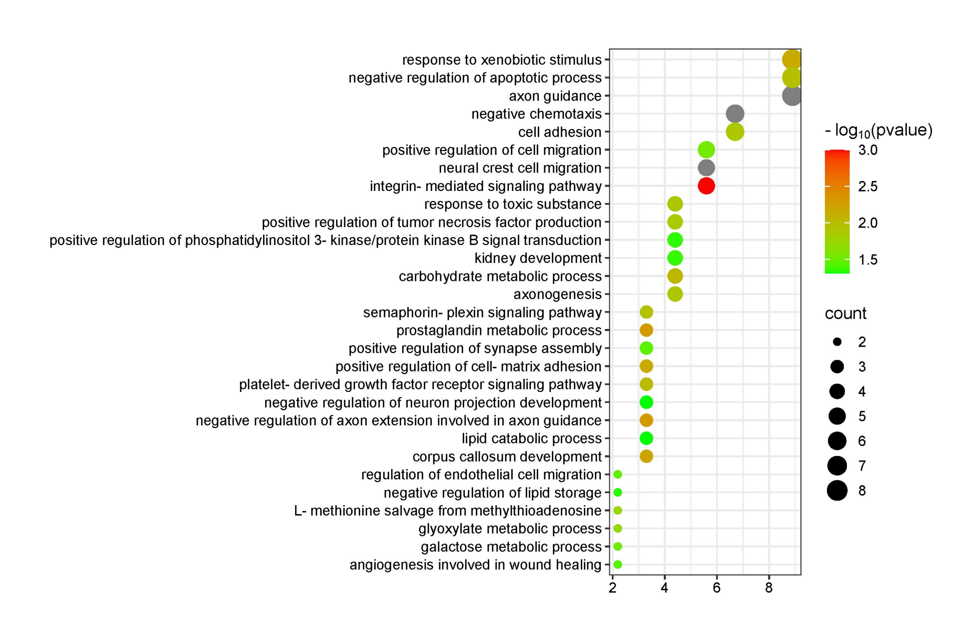


图 2 橄榄油组与对照组差异蛋白富集到的生物学过程

3.2.3 黄油组尿液蛋白质组成组分析

3.2.3.1 差异蛋白

将黄油组（C 组）与对照组（A 组）尿液蛋白质进行比较，筛选差异蛋白条件为：变化倍数 FC ≥ 1.5 或 ≤ 0.67，双尾配对 t 检验 $P < 0.05$。结果表明，相对于对照组，黄油组共鉴定到 89 个差异蛋白，其中 15 种下调，74 种上调。将差异蛋白按 FC 由小到大的顺序排列，通过 Uniprot 进行检索，详细信息列于表 4。

表 4 黄油组与对照组以 FC≥1.5 或≤0.67，P<0.05 筛选的尿蛋白质组差异蛋白

Uniprot ID	Protein name	Fold change	P-value	Trend
P14844	C-C motif chemokine 2	0.190	2.18E-02	↓
M0R7T1	Phosphatase and actin regulator 4	0.239	4.91E-02	↓
A0A0G2JXY4	Carbonic anhydrase 15	0.258	4.02E-02	↓
Q812E9	Neuronal membrane glycoprotein M6-a	0.277	2.56E-02	↓

P25236	Selenoprotein P	0.340	2.72E-04	↓
P34058	Heat shock protein HSP 90-beta	0.351	1.10E-02	↓
Q9JJ40	Na(+)/H(+) exchange regulatory cofactor NHE-RF3	0.364	1.70E-02	↓
B4F7A5	Cd99 protein	0.412	1.17E-02	↓
A0A0G2JXZ9	protein-tyrosine-phosphatase	0.415	1.41E-02	↓
F8WG88	Follistatin-related protein 1	0.484	3.68E-02	↓
Q5M876	N-acyl-aromatic-L-amino acid amidohydrolase	0.508	1.56E-02	↓
Q8R2H2	Integrin beta-3	0.509	1.98E-02	↓
D3Z9U8	S100 calcium binding protein A7 like 2	0.542	2.15E-02	↓
G3V6A0	Platelet-derived growth factor receptor alpha	0.603	3.98E-02	↓
Q5HZW5	CD320 antigen	0.668	2.51E-02	↓
P04785	Protein disulfide-isomerase	1.600	1.80E-02	↑
F1LPC6	Carboxypeptidase D	1.673	2.01E-02	↑
D3ZZ44	Extracellular leucine-rich repeat and fibronectin type III domain containing 1	1.713	1.37E-03	↑
D3ZQP6	Semaphorin 7A	1.740	1.47E-02	↑
Q00657	Chondroitin sulfate proteoglycan 4	1.769	4.27E-02	↑
A0A0G2JTX5	Dipeptidyl peptidase 4	1.817	3.56E-02	↑
M0RDA4	receptor protein-tyrosine kinase	1.865	2.60E-02	↑
P47820	Angiotensin-converting enzyme	1.969	2.16E-02	↑
Q5M843	2-oxoglutarate and iron-dependent oxygenase domain-containing protein 3	2.027	3.65E-02	↑
G3V989	EPH-related receptor tyrosine kinase ligand 7	2.033	1.78E-02	↑
Q6JE36	Protein NDRG1	2.076	3.64E-02	↑
G3V8P3	Cadherin, EGF LAG seven-pass G-type receptor 2	2.091	2.43E-02	↑
M0R3V4	Myeloid-derived growth factor	2.139	1.61E-02	↑
F1MAA7	Laminin subunit gamma 1	2.177	1.40E-02	↑
A0A0G2JV12	Collagen type XV alpha 1 chain	2.241	1.76E-02	↑
A0A0G2K0Q8	Sushi domain containing 2	2.251	1.66E-02	↑

P16975	SPARC	2.328	2.02E-02	↑
A0A0G2JY48	receptor protein-tyrosine kinase	2.334	1.67E-03	↑
Q3MHS9	T-complex protein 1 subunit zeta	2.336	3.94E-02	↑
E9PSU8	Ig-like domain-containing protein	2.338	1.73E-02	↑
P61972	Nuclear transport factor 2	2.346	2.42E-02	↑
Q09326	Alpha-1,6-mannosyl-glycoprotein 2-beta-N-acetylglucosaminyltransferase	2.405	3.67E-02	↑
B2RYC9	Glucosylceramidase	2.417	2.38E-02	↑
A0A140TAI2	Biotinidase	2.447	6.64E-03	↑
F1LSV0	Semaphorin 4B	2.478	3.81E-02	↑
F1LMM4	Protein kinase domain containing, cytoplasmic	2.481	4.74E-02	↑
G3V6H1	Galactocerebrosidase	2.490	1.41E-02	↑
D3ZBN3	receptor protein-tyrosine kinase	2.496	3.87E-02	↑
P27867	Sorbitol dehydrogenase	2.541	2.72E-02	↑
G3V7W1	Programmed cell death protein 6	2.595	2.93E-02	↑
P00731	Carboxypeptidase A1	2.686	4.49E-02	↑
P05197	Elongation factor 2	2.839	3.13E-02	↑
B1WBV2	Secreted frizzled-related protein 2	2.917	1.49E-02	↑
Q5U367	Multifunctional procollagen lysine hydroxylase and glycosyltransferase LH3 [Includes: Procollagen-lysine,2-oxoglutarate 5-dioxygenase 3	2.983	2.14E-02	↑
D3ZAN3	Glucosidase II alpha subunit	3.074	1.21E-02	↑
D3ZBB2	deleted	3.255	1.13E-02	↑
P45479	Palmitoyl-protein thioesterase 1	3.266	1.42E-02	↑
O35142	Coatomer subunit beta'	3.325	2.60E-02	↑
B5DEI2	Amine oxidase	3.407	1.62E-02	↑
B1H232	Immunoglobulin superfamily containing leucine-rich repeat	3.410	8.35E-03	↑
P04905	Glutathione S-transferase Mu 1	3.442	3.66E-02	↑
Q562C9	Acireductone dioxygenase	3.475	4.93E-03	↑

Q80WD1	Reticulon-4 receptor-like 2	3.557	4.87E-03	↑
D3ZE93	CEA cell adhesion molecule 19	3.606	1.88E-02	↑
Q920A6	Retinoid-inducible serine carboxypeptidase	3.715	3.39E-03	↑
Q66H12	Alpha-N-acetylgalactosaminidase	3.730	4.56E-03	↑
F1LP42	Hedgehog protein	4.034	4.13E-03	↑
A0A0H2UHH2	Amyloid P component, serum	4.067	1.05E-03	↑
G3V827	Kynurenine aminotransferase 1	4.172	4.31E-02	↑
Q9Z339	Glutathione S-transferase omega-1	4.176	1.84E-02	↑
Q4FZV0	Beta-mannosidase	4.251	9.96E-03	↑
O35760	Isopentenyl-diphosphate Delta-isomerase 1	4.294	2.14E-02	↑
A2IBE0	Membrane-bound carbonic anhydrase 14	4.436	8.45E-03	↑
M0RAM5	Glutathione peroxidase	4.455	3.51E-02	↑
Q9EQV6	Tripeptidyl-peptidase 1	4.803	4.37E-04	↑
Q8R5M3	Leucine-rich repeat-containing protein 15	5.157	4.21E-04	↑
P84039	Ectonucleotide pyrophosphatase/phosphodiesterase family member 5	5.291	4.31E-03	↑
Q99M75	Reticulon-4 receptor	5.372	3.36E-02	↑
F1M7B3	Ig-like domain-containing protein	5.421	7.84E-03	↑
G3V862	Angiopoietin-like 2	5.789	8.65E-03	↑
Q5PPH0	Enolase-phosphatase E1	5.794	4.31E-02	↑
Q32KJ6	N-acetylgalactosamine-6-sulfatase	5.809	2.21E-02	↑
Q5I0D5	Phospholysine phosphohistidine inorganic pyrophosphate phosphatase	6.164	1.55E-02	↑
D3ZXJ0	Matrix metallopeptidase 17	6.260	4.42E-02	↑
B2GUX7	Cellular repressor of E1A-stimulated genes 1	6.517	3.59E-02	↑
F1M3Y4	RCG64257-like	7.480	4.96E-02	↑
A0A0G2K5X3	deleted	7.517	3.25E-02	↑
Q5FVH2	5'-3' exonuclease PLD3	7.683	1.16E-02	↑
P53369	Oxidized purine nucleoside triphosphate hydrolase	9.404	5.06E-03	↑

D3ZP44	SLIT and NTRK-like family, member 6	10.530	4.31E-02	↑
F1M091	Kallikrein m	15.790	4.14E-02	↑
Q99ML5	Prenylcysteine oxidase 1	17.347	4.97E-02	↑
Q5M819	Phosphoserine phosphatase	34.176	2.31E-02	↑
P48032	Metalloproteinase inhibitor 3	306.177	1.05E-02	↑

3.2.3.2 差异蛋白功能分析

将鉴定到的差异蛋白于 Pubmed 数据库进行文献检索。

黄油组与橄榄油组中部分差异蛋白相同，如 Heat shock protein HSP 90-beta、Glutathione peroxidase、Oxidized purine nucleoside triphosphate hydrolase 等。

在其他黄油组的下调的差异蛋白中：C-C motif chemokine 2 (FC=0.190, P= 2.18E-02)在心血管疾病的发病机制中起主要作用，其下调被认为是他汀类药物的多效性特性之一[21]。Neuronal membrane glycoprotein M6-a (FC=0.277, P= 2.56E-02)在激活 Src/MAPK/ERK、PKC 和 PI3K/AKT、Rufy3-Rap2-STEF/Tiam2 信号通路中发挥重要作用，分别促进神经突生长和神经元极化，还参与树突棘的形成和成熟[22]。Selenoprotein P (FC=0.340, P= 2.72E-04)作为主要的硒转运蛋白维持着大脑充足的硒供应，对于大脑的正常发育和功能至关重要，并且还可能与中枢神经系统的病理过程有关，具有抗氧化活性[23]。

在上调的蛋白中：Metalloproteinase inhibitor 3 (FC=306.177, P= 1.05E-02)的上调幅度最大，研究发现 TIMP3 过表达抑制了与代谢炎症和应激相关的途径，包括 Jun NH2 末端激酶和 p38 激酶的激活，减少了氧化应激信号的激活，与脂质过氧化、蛋白质羰基化和硝化有关[24]。Prenylcysteine oxidase 1 (FC=17.347, P= 4.97E-02)活性升高可能会导致过氧化氢增加，进而增加传播低密度脂蛋白时的氧化负担，因此该蛋白可作为心血管疾病的潜在药物靶点和新的生物标志物[25]。Cellular repressor of E1A-stimulated genes 1 (FC=6.517, P= 3.59E-02)可能调节血管壁细胞的稳态并抑制血管组织细胞和巨噬细胞的炎症，对炎症具有潜在的保护作用[26]。Palmitoyl-protein thioesterase 1 (FC=3.266, P= 1.42E-02)在高脂肪饮食的大鼠中表达上调，其表达的增加可能对精子发生过程中的支持细胞功能有害[27]。

3.2.3.3 差异蛋白富集生物学过程分析

使用 DAVID 数据库对成组分析鉴定到的 89 个差异蛋白进行生物学过程（Biological process, BP）富集分析。结果显示，共有 40 个 BP 通路被显著富集（$P<0.05$），详细信息列

于图 3。

与橄榄油组相同的是，黄油组也富集到了很多与神经系统相关的通路，包括轴突导向、胼胝体发育、神经嵴细胞迁移等。此外，黄油组富集到了部分代谢相关通路，如蛋白水解、谷胱甘肽代谢过程、对营养水平的反应、蛋白质代谢过程的负调控。

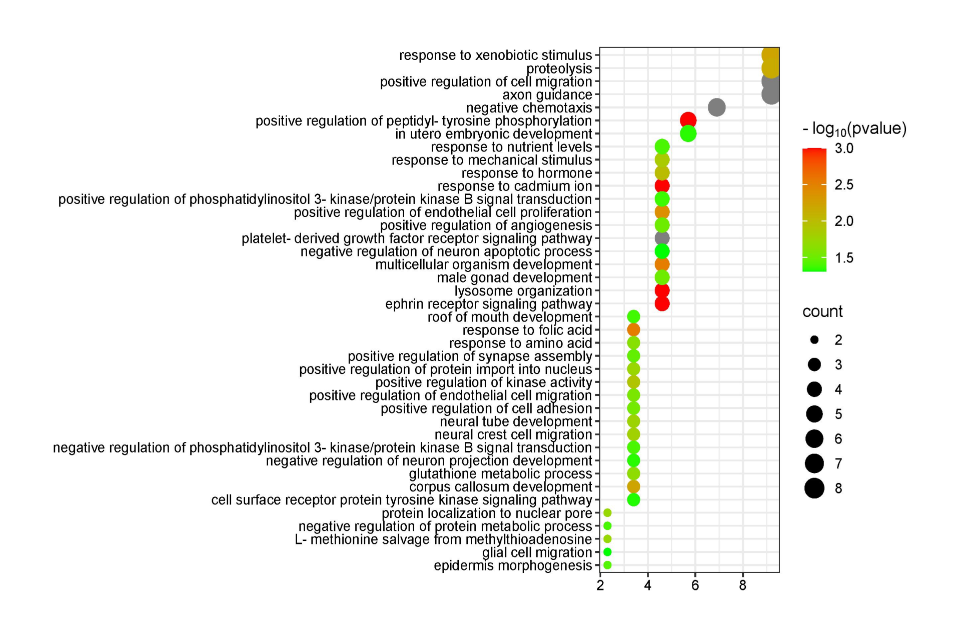


图 3 黄油组与对照组差异蛋白富集到的生物学过程

3.2.4 猪油组尿液蛋白质组成组分析

3.2.4.1 差异蛋白

将猪油组（D 组）与对照组（A 组）尿液蛋白质进行比较，筛选差异蛋白条件为：变化倍数 $FC \geq 1.5$ 或 ≤ 0.67，双尾配对 t 检验 $P < 0.05$。结果表明，相对于对照组，猪油组共鉴定到 104 个差异蛋白，其中 25 种下调，79 种上调。将差异蛋白按 FC 由小到大的顺序排列，通过 Uniprot 进行检索，详细信息列于表 5。

表 5 猪油组与对照组以 FC≥1.5 或≤0.67，P<0.05 筛选的尿蛋白质组差异蛋白

Uniprot ID	Protein name	Fold change	P-value	Trend
P21708	Mitogen-activated protein kinase 3	0.000	2.67E-02	↓
A0A0G2K1V9	deleted	0.017	2.51E-02	↓
Q66H69	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 7	0.020	4.93E-02	↓

F1LMP1	Alpha-1,3-mannosyl-glycoprotein 4-beta-N-acetylglucosaminyltransferase A	0.036	3.30E-02	↓
F1M3T3	deleted	0.059	2.98E-02	↓
P18614	Integrin alpha-1	0.080	3.00E-02	↓
P35467	Protein S100-A1	0.111	2.99E-02	↓
B1H219	Dickkopf WNT signaling pathway inhibitor 3	0.120	4.74E-02	↓
Q63434	Placenta growth factor	0.158	4.47E-02	↓
D3ZPM7	ADAM metallopeptidase domain 19	0.160	2.52E-02	↓
A0A0G2JXY4	Carbonic anhydrase 15	0.160	2.14E-02	↓
P14844	C-C motif chemokine 2	0.174	2.49E-02	↓
Q68FR6	Elongation factor 1-gamma	0.175	2.04E-02	↓
Q5U206	Calmodulin-like protein 3	0.298	4.67E-02	↓
B4F7A5	Cd99 protein	0.345	3.26E-02	↓
Q9JIK1	Cadherin-related family member 5	0.385	2.81E-02	↓
P34058	Heat shock protein HSP 90-beta	0.425	3.00E-02	↓
A0A0G2JXZ9	protein-tyrosine-phosphatase	0.427	1.75E-02	↓
A0A0G2K872	Cell adhesion molecule 3	0.451	2.82E-02	↓
Q9EPF2	Cell surface glycoprotein MUC18	0.498	4.69E-02	↓
P25236	Selenoprotein P	0.515	3.25E-02	↓
D3Z9U8	S100 calcium binding protein A7 like 2	0.525	3.42E-02	↓
G3V6A0	Platelet-derived growth factor receptor alpha	0.538	4.91E-02	↓
D4A6K7	Leucine rich repeat containing 19	0.580	2.03E-02	↓
P08289	Alkaline phosphatase, tissue-nonspecific isozyme	0.617	4.42E-02	↓
B2RYB8	Integrin beta	1.541	9.73E-03	↑
Q9WVH8	Fibulin-5	1.584	4.17E-02	↑
G3V7L8	V-type proton ATPase subunit E 1	1.681	4.81E-03	↑
A0A0G2KB31	Hepsin	1.734	3.77E-03	↑
P25113	Phosphoglycerate mutase 1	1.862	9.98E-03	↑
M0R3V4	Myeloid-derived growth factor	1.916	4.70E-02	↑

P80254	D-dopachrome decarboxylase	1.929	1.74E-02	↑
P85971	6-phosphogluconolactonase	1.997	3.14E-02	↑
D4AC39	Fibronectin leucine rich transmembrane protein 1	2.016	3.09E-02	↑
Q63530	Phosphotriesterase-related protein	2.025	1.44E-02	↑
F1LSV0	Semaphorin 4B	2.032	1.85E-02	↑
A0A0G2JU82	Microtubule-actin crosslinking factor 1	2.102	2.80E-02	↑
Q711G3	Isoamyl acetate-hydrolyzing esterase 1 homolog	2.103	1.19E-02	↑
A0A140TAI2	Biotinidase	2.114	1.04E-02	↑
Q5XI77	Annexin	2.204	1.63E-02	↑
P13265	Glypican-3	2.230	2.23E-02	↑
P19804	Nucleoside diphosphate kinase B	2.281	1.78E-02	↑
P63322	Ras-related protein Ral-A	2.289	7.84E-03	↑
Q32KK2	Arylsulfatase A	2.304	4.07E-03	↑
O35142	Coatomer subunit beta'	2.320	4.96E-02	↑
A0A0G2JSJ8	Alpha-L-fucosidase	2.376	1.81E-02	↑
F1M8B7	Charged multivesicular body protein 2B	2.480	9.79E-03	↑
P61972	Nuclear transport factor 2	2.494	2.47E-04	↑
M0RAM5	Glutathione peroxidase	2.506	2.23E-03	↑
Q9Z339	Glutathione S-transferase omega-1	2.522	3.47E-02	↑
Q8CGS4	Charged multivesicular body protein 3	2.538	1.74E-02	↑
Q3MIE4	Synaptic vesicle membrane protein VAT-1 homolog	2.538	2.27E-02	↑
Q5BK81	Prostaglandin reductase 2	2.557	2.02E-02	↑
O35760	Isopentenyl-diphosphate Delta-isomerase 1	2.680	3.10E-02	↑
Q6IMK4	Amine oxidase	2.722	4.54E-02	↑
G3V7W1	Programmed cell death protein 6	2.745	2.27E-03	↑
G3V6H1	Galactocerebrosidase	2.852	1.20E-02	↑
Q5XI89	NXPE family member 4	2.876	8.73E-03	↑
G3V8T4	DNA damage-binding protein 1	2.878	2.68E-02	↑
G3V8P3	Cadherin, EGF LAG seven-pass G-type receptor 2	2.891	2.80E-02	↑

G3V722	Beta-1,4-galactosyltransferase	2.921	3.98E-02	↑
Q5U367	Multifunctional procollagen lysine hydroxylase and glycosyltransferase LH3 [Includes: Procollagen-lysine,2-oxoglutarate 5-dioxygenase 3	2.973	2.87E-03	↑
B1H232	Immunoglobulin superfamily containing leucine-rich repeat	2.976	1.25E-03	↑
P08010	Glutathione S-transferase Mu 2	3.188	2.56E-02	↑
B0BNL6	Arrestin domain-containing protein 1	3.191	2.27E-02	↑
P02651	Apolipoprotein A-IV	3.246	4.63E-02	↑
Q99M75	Reticulon-4 receptor	3.285	9.57E-03	↑
D3Z9E1	Elastin microfibril interfacer 1	3.338	2.03E-02	↑
P08753	Guanine nucleotide-binding protein G	3.354	3.85E-02	↑
Q66H12	Alpha-N-acetylgalactosaminidase	3.454	2.90E-02	↑
P84039	Ectonucleotide pyrophosphatase/phosphodiesterase family member 5	3.457	3.43E-02	↑
Q64057	Alpha-aminoadipic semialdehyde dehydrogenase	3.567	2.53E-02	↑
A0A0H2UHH2	Amyloid P component, serum	3.582	1.07E-03	↑
Q99MF4	Interleukin-11 receptor subunit alpha	3.611	9.95E-03	↑
Q920A6	Retinoid-inducible serine carboxypeptidase	3.837	2.78E-02	↑
G3V7N8	Galectin 9	3.996	4.84E-02	↑
Q32KJ6	N-acetylgalactosamine-6-sulfatase	3.997	2.82E-02	↑
P22734	Catechol O-methyltransferase	4.360	2.81E-02	↑
A0A0G2K828	Ig-like domain-containing protein	4.406	3.31E-02	↑
B2GUX7	Cellular repressor of E1A-stimulated genes 1	4.482	2.15E-03	↑
D3ZC04	Extended synaptotagmin 3	4.681	4.39E-03	↑
Q8R5M3	Leucine-rich repeat-containing protein 15	4.748	3.96E-02	↑
A2IBE0	Membrane-bound carbonic anhydrase 14	4.763	1.32E-02	↑
D4ACR1	RCG64219-like	5.020	3.70E-02	↑

Q5I0D5	Phospholysine phosphohistidine inorganic pyrophosphate phosphatase	5.063	1.30E-02	↑
A0A0G2KAY8	Selenoprotein F	5.094	2.71E-02	↑
Q9EQV6	Tripeptidyl-peptidase 1	5.099	6.49E-04	↑
A0A0G2K4B4	acid phosphatase	5.532	4.62E-02	↑
Q5PPH0	Enolase-phosphatase E1	5.755	2.11E-02	↑
D4A4U3	Magnesium-dependent phosphatase 1	6.335	1.78E-02	↑
Q6IE17	Stefin A2-like 1	6.491	4.71E-02	↑
Q5FVH2	5'-3' exonuclease PLD3	6.568	2.80E-03	↑
P06214	Delta-aminolevulinic acid dehydratase	7.207	1.92E-02	↑
Q8R5M5	2-amino-3-carboxymuconate-6-semialdehyde decarboxylase	7.322	1.31E-03	↑
A0A0G2JSZ5	Protein disulfide-isomerase A6	8.080	4.80E-02	↑
Q8CJ52	Prominin-2	8.125	4.53E-02	↑
D3ZTV3	Leucine-rich repeat transmembrane protein FLRT2	8.840	3.17E-02	↑
P53369	Oxidized purine nucleoside triphosphate hydrolase	9.126	5.87E-04	↑
B2GV72	Carbonyl reductase [NADPH] 3	11.616	8.39E-04	↑
P03994	Hyaluronan and proteoglycan link protein 1	13.005	5.51E-03	↑
A0A0G2K0W3	Protein tweety homolog	13.487	1.93E-02	↑
Q5M819	Phosphoserine phosphatase	25.782	8.88E-03	↑
P02696	Retinol-binding protein 1	38.811	3.04E-02	↑
P81556	Metalloproteinase inhibitor 4	85.055	3.60E-02	↑

3.2.4.2 差异蛋白功能分析

将鉴定到的差异蛋白于 Pubmed 数据库进行文献检索。

在猪油组下调的差异蛋白中：Mitogen-activated protein kinase 3 (FC=0, P= 2.67E-02)可能在神经元的功能调节中扮演着重要角色，其对 mGlu5 受体的调控参与了多种神经生物学过程，如突触可塑性、学习和记忆等[28]。Protein S100-A1 (FC=0.111, P= 2.99E-02)在结合钙时

会发生大的构象变化，以与众多蛋白质靶标相互作用，包括参与钙信号传导的蛋白质、神经递质释放（synapsins I 和 II）、细胞骨架等[29]。Dickkopf WNT signaling pathway inhibitor 3 (FC=0.120, P= 4.74E-02)在阿尔茨海默病患者和阿尔茨海默病转基因小鼠模型的脑组织中表达显著降低[30]。

在上调的差异蛋白中：上调幅度最大的蛋白为Metalloproteinase inhibitor 4 (FC=85.055, P= 3.60E-02)属于细胞外基质金属蛋白酶抑制剂家族，在多种癌症中过表达，目前还未有其与猪油摄入相关的研究[31]。Retinol-binding protein 1 (FC=38.811, P= 3.04E-02)作为一种伴侣蛋白调节视黄醇的摄取、随后的酯化和生物利用度，并可以通过与细胞膜受体相互作用将维生素A 输送到细胞[32][33]。Hyaluronan and proteoglycan link protein 1 (FC=13.005, P= 5.51E-03)通过刺激 Nrf2/ARE 途径抑制 NLRP3 炎症小体，从而抑制神经炎症、增强运动神经元存活，并改善脊髓损伤后的神经功能恢复[34]。Prominin-2 (FC=8.125, P= 4.53E-02)是由铁死亡刺激诱导的，并可以起到抵抗铁死亡的作用[35]。Protein disulfide-isomerase A6 (FC=8.080, P= 4.80E-02) 与脊髓损伤修复相关，还被发现可促进受损神经元修复[36]。2-amino-3-carboxymuconate-6-semialdehyde decarboxylase (FC=7.322, P= 1.31E-03)在色氨酸分解代谢中起着关键作用，是治疗与色氨酸代谢物水平升高相关疾病的有吸引力的治疗靶点[37]。

3.2.4.3 差异蛋白富集生物学过程分析

使用 DAVID 数据库对成组分析鉴定到的 104 个差异蛋白进行生物学过程（Biological process, BP）富集分析。结果显示，共有 32 个 BP 通路被显著富集（P<0.05），详细信息列于图 4。

在富集到的通路中，含有部分与代谢相关的通路，包括对脂多糖的反应、脂质代谢过程、糖苷分解代谢过程、谷胱甘肽代谢过程。而在橄榄油组和黄油组中大量出现的神经系统相关通路并没有出现。

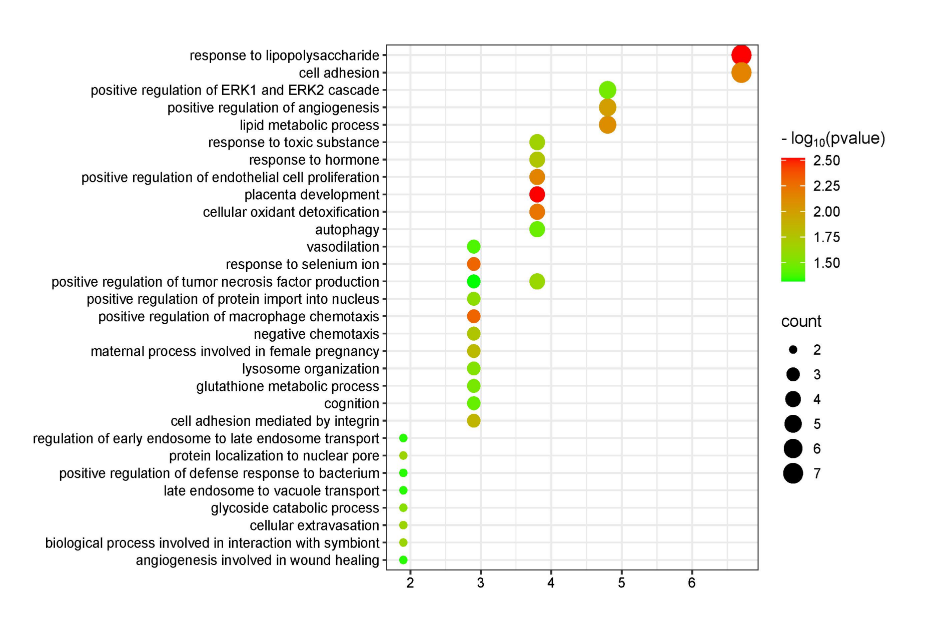


图 4 猪油组与对照组差异蛋白富集到的生物学过程

3.2.5 氢化植物油组尿液蛋白质组成组分析

3.2.5.1 差异蛋白

将氢化植物油组（E 组）与对照组（A 组）尿液蛋白质进行比较，筛选差异蛋白条件为：变化倍数 FC ≥ 1.5 或 ≤ 0.67，双尾配对 t 检验 P < 0.05。结果表明，相对于对照组，氢化植物油组共鉴定到 63 个差异蛋白，其中 34 种下调，29 种上调。将差异蛋白按 FC 由小到大的顺序排列，通过 Uniprot 进行检索，详细信息列于表 6。

表 6 氢化植物油组与对照组以 FC≥1.5 或≤0.67，P<0.05 筛选的尿蛋白质组差异蛋白

Uniprot ID	Protein name	Fold change	P-value	Trend
F1LMP9	Disabled homolog 2	0.000	4.72E-02	↓
Q5U206	Calmodulin-like protein 3	0.011	4.55E-02	↓
P18614	Integrin alpha-1	0.036	2.67E-02	↓
F1LMP1	Alpha-1,3-mannosyl-glycoprotein 4-beta-N-acetylglucosaminyltransferase A	0.041	4.72E-02	↓
F1M3T3	deleted	0.074	3.16E-02	↓
Q5XIF6	Tubulin alpha-4A chain	0.087	4.61E-02	↓
A0A0G2K0V8	Nuclear distribution C, dynein complex regulator	0.091	3.39E-02	↓
P81155	Voltage-dependent anion-selective channel protein 2	0.092	2.31E-02	↓
F1LM19	Alpha-2-HS-glycoprotein	0.116	4.48E-02	↓

Q62662	Tyrosine-protein kinase FRK	0.142	4.75E-02	↓
D3ZV56	Ring finger protein 150	0.165	4.24E-02	↓
P14844	C-C motif chemokine 2	0.186	2.09E-02	↓
Q8K4G9	Podocin	0.187	4.54E-02	↓
D4A2Z2	Eppin	0.192	2.36E-02	↓
Q62975	Protein Z-dependent protease inhibitor	0.197	3.62E-02	↓
Q8R2H2	Integrin beta-3	0.287	2.57E-02	↓
Q63434	Placenta growth factor	0.306	2.35E-02	↓
P41498	Low molecular weight phosphotyrosine protein phosphatase	0.320	4.89E-02	↓
A0A0G2K2L1	deleted	0.329	3.89E-02	↓
P16296	Coagulation factor IX	0.357	3.56E-02	↓
F1M8E9	lysozyme	0.368	2.26E-02	↓
Q63768	Adapter molecule crk	0.407	3.13E-02	↓
Q3T1J1	Eukaryotic translation initiation factor 5A-1	0.417	4.90E-02	↓
A0A0G2K7Y0	CD46 molecule	0.429	3.01E-02	↓
Q9QYL8	Acyl-protein thioesterase 2	0.438	5.51E-03	↓
Q99PW7	Follistatin-related protein 3	0.441	1.67E-02	↓
A0A0G2K676	chitinase	0.442	2.87E-02	↓
P02680	Fibrinogen gamma chain	0.475	4.45E-02	↓
F1LQT4	Carboxypeptidase N subunit 2	0.480	2.41E-02	↓
Q9EPF2	Cell surface glycoprotein MUC18	0.522	3.91E-02	↓
G3V7Y3	ATP synthase F1 subunit delta	0.533	3.87E-02	↓
D3ZCH9	CD177 molecule	0.541	4.60E-02	↓
Q99J86	Attractin	0.577	6.75E-03	↓
G3V6K1	Transcobalamin-2	0.591	2.26E-02	↓
Q9QX71	Napsin	1.549	1.57E-02	↑
P85971	6-phosphogluconolactonase	1.640	3.52E-02	↑
Q80ZA3	Serine	1.699	4.24E-02	↑
F1M1R0	Similar to immunoglobulin light chain variable region	1.788	3.80E-02	↑

F1LSV0	Semaphorin 4B	1.847	3.57E-02	↑
B2RYC9	Glucosylceramidase	1.865	3.69E-02	↑
D3ZC04	Extended synaptotagmin 3	2.014	3.45E-02	↑
P02651	Apolipoprotein A-IV	2.120	2.91E-02	↑
A0A0H2UHQ0	Solute carrier family 3 member 2	2.145	3.79E-02	↑
Q562C9	Acireductone dioxygenase	2.276	2.49E-02	↑
Q80WD1	Reticulon-4 receptor-like 2	2.365	3.08E-02	↑
D3ZAN3	Glucosidase II alpha subunit	2.365	2.30E-02	↑
Q99MF4	Interleukin-11 receptor subunit alpha	2.603	2.19E-02	↑
Q64573	Liver carboxylesterase 1F	2.625	4.17E-02	↑
G3V862	Angiopoietin-like 2	2.626	3.13E-02	↑
O35760	Isopentenyl-diphosphate Delta-isomerase 1	2.763	3.37E-02	↑
Q64361	Latexin	2.916	3.41E-02	↑
A0A0G2K0Q8	Sushi domain containing 2	3.023	3.66E-02	↑
A0A0H2UHH2	Amyloid P component, serum	3.156	3.78E-02	↑
D4AA31	Prolylcarboxypeptidase	3.491	3.78E-02	↑
B0BN46	Grhpr protein	3.681	1.92E-02	↑
Q9EQV6	Tripeptidyl-peptidase 1	3.706	4.88E-02	↑
E9PSU8	Ig-like domain-containing protein	3.714	3.60E-02	↑
P22734	Catechol O-methyltransferase	3.841	2.40E-02	↑
M0R936	Ig-like domain-containing protein	4.155	4.81E-02	↑
Q5FVH2	5'-3' exonuclease PLD3	4.715	2.20E-02	↑
D4A4U3	Magnesium-dependent phosphatase 1	5.130	2.60E-02	↑
Q8R5M5	2-amino-3-carboxymuconate-6-semialdehyde decarboxylase	10.148	2.71E-02	↑
Q5M819	Phosphoserine phosphatase	14.636	4.44E-02	↑

3.2.5.2 差异蛋白功能分析

将鉴定到的差异蛋白于 Pubmed 数据库进行文献检索。

在氢化植物油组下调的差异蛋白中：Disabled homolog 2 (FC=0, P= 4.72E-02)在控制巨噬细胞表型极化和脂肪组织炎症中起着关键作用，其缺陷会导致脂肪组织炎症加剧和胰岛素抵抗[38]。Calmodulin-like protein 3 (FC=0.011, P= 4.55E-02)基因敲除的肌肉表现出了钙释放减弱、钙调蛋白激酶信号减少以及肌肉对运动的适应性受损[39]。Integrin alpha-1 (FC=0.036, P= 2.67E-02)在高脂饮食挑战下可以促进肝脏胰岛素作用，并同时促进脂质积累，在肝脏代谢中发挥作用；其缺失会改变高脂饮食小鼠的脂肪酸代谢，改善脂肪肝情况[40]。Alpha-2-HS-glycoprotein (FC=0.116, P= 4.48E-02)是一种主要在肝脏合成的多功能血浆糖蛋白，被认为是多种正常和病理过程的重要组成部分，包括骨代谢调节、血管钙化、胰岛素抵抗和蛋白酶活性控制，在肥胖及相关并发症（如 2 型糖尿病、代谢综合征和非酒精性脂肪肝病）过程中，循环中的 Alpha-2-HS-glycoprotein 显著升高[41]。Eppin (FC=0.192, P= 2.36E-02)是人类精液中雄激素作用的生物标志物，研究发现其与精液质量、精子活力等密切相关，Eppin 表达下调会使精子运动能力显著下降[42]。

在上调的差异蛋白中：Phosphoserine phosphatase (FC=14.636, P= 4.44E-02)为上调幅度最大的蛋白，暂无文献研究显示其与代谢活动的相关性。Catechol O-methyltransferase (FC=3.841, P= 2.40E-02)在代谢多巴胺方面起着关键作用，该蛋白基因中的常见功能多态性会影响与前额叶皮层相关的认知功能、睡眠-觉醒调节，并可能影响睡眠病理[43]。

3.2.5.3 差异蛋白富集生物学过程分析

使用 DAVID 数据库对成组分析鉴定到的 63 个差异蛋白进行生物学过程（Biological process, BP）富集分析。结果显示，共有 16 个 BP 通路被显著富集（$P<0.05$），详细信息列于图 5。

在富集到的通路中，含有部分与代谢相关的通路，包括碳水化合物代谢过程、乙醛酸酯代谢过程、代谢过程。同样不含有在橄榄油组和黄油组中大量出现的神经系统相关通路。

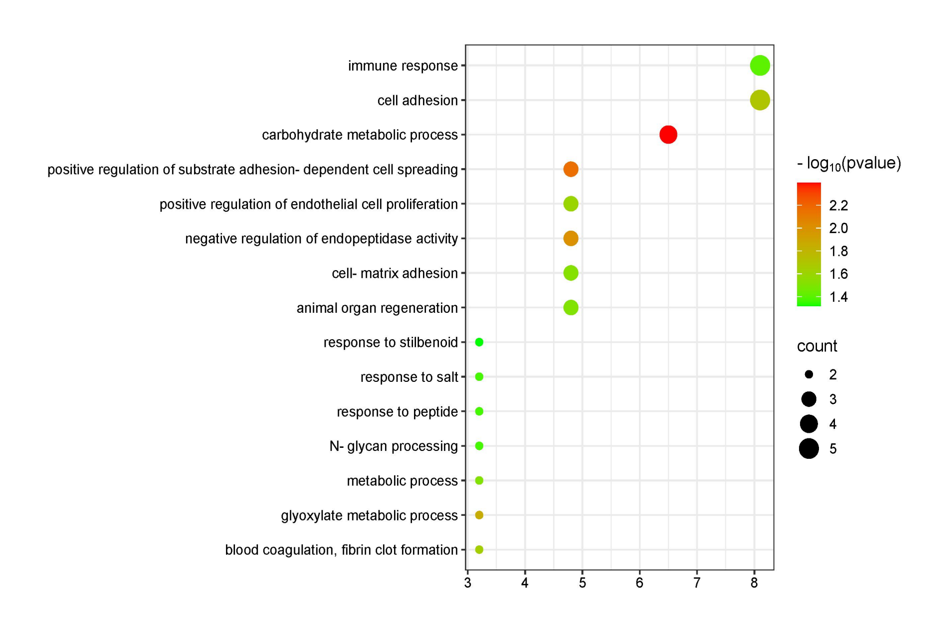


图 5 氢化植物油组与对照组差异蛋白富集到的生物学过程

3.2.6 菜籽油组尿液蛋白质组成组分析

3.2.6.1 差异蛋白

将菜籽油组（F 组）与对照组（A 组）尿液蛋白质进行比较，筛选差异蛋白条件为：变化倍数 FC ≥ 1.5 或 ≤ 0.67，双尾配对 t 检验 P < 0.05。结果表明，相对于对照组，菜籽油组共鉴定到 105 个差异蛋白，其中 53 种下调，52 种上调。将差异蛋白按 FC 由小到大的顺序排列，通过 Uniprot 进行检索，详细信息列于表 7。

表 7 菜籽油组与对照组以 FC≥1.5 或≤0.67，P<0.05 筛选的尿蛋白质组差异蛋白

Uniprot ID	Protein name	Fold change	P-value	Trend
A0A096MIU6	Fc fragment of IgG receptor IIa	0.000	4.14E-02	↓
A0A0G2JTL4	Mast/stem cell growth factor receptor	0.000	3.33E-02	↓
A0A0G2K0V8	Nuclear distribution C, dynein complex regulator	0.000	2.81E-02	↓
A0A0G2K7L8	Thrombospondin 4	0.000	4.46E-02	↓
D3ZM36	Interleukin 10 receptor subunit beta	0.000	2.63E-02	↓
D3ZV56	Ring finger protein 150	0.000	2.83E-02	↓
D3ZW55	Inosine triphosphate pyrophosphatase	0.000	4.44E-02	↓
D4A740	Interleukin 17 receptor A	0.000	2.50E-02	↓
D4ACX8	Protocadherin-16	0.000	4.93E-02	↓

F1LMP9	Disabled homolog 2	0.000	4.72E-02	↓
F1LW74	IQ motif containing GTPase activating protein 2	0.000	2.72E-02	↓
F1M7W8	deleted	0.000	2.65E-02	↓
P16975	SPARC	0.000	4.05E-02	↓
P18614	Integrin alpha-1	0.000	2.42E-02	↓
P35467	Protein S100-A1	0.000	3.86E-02	↓
Q4V8I1	Endothelial protein C receptor	0.000	3.81E-02	↓
Q5XIF6	Tubulin alpha-4A chain	0.000	3.68E-02	↓
Q5XIN7	Protein O-linked-mannose beta-1,2-N-acetylglucosaminyltransferase 1	0.000	3.26E-02	↓
Q66H69	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 7	0.000	4.89E-02	↓
Q9ES58	Cell surface glycoprotein CD200 receptor 1	0.000	4.12E-02	↓
Q63434	Placenta growth factor	0.000	3.27E-02	↓
Q5U206	Calmodulin-like protein 3	0.002	4.41E-02	↓
F1LMP1	Alpha-1,3-mannosyl-glycoprotein 4-beta-N-acetylglucosaminyltransferase A	0.016	3.58E-02	↓
A0A0G2JVV1	C-type lectin domain family 2, member G	0.040	1.77E-02	↓
P70549	Sodium/calcium exchanger 3	0.044	4.00E-02	↓
Q9ES53	Ubiquitin recognition factor in ER-associated degradation protein 1	0.047	2.33E-02	↓
D3ZPM7	ADAM metallopeptidase domain 19	0.047	2.18E-02	↓
Q5I0D1	Glyoxalase domain-containing protein 4	0.050	4.90E-02	↓
Q62975	Protein Z-dependent protease inhibitor	0.057	2.61E-02	↓
A0A0G2KA95	L1 cell adhesion molecule	0.059	2.42E-02	↓
A0A0G2JZ40	Reversion-inducing-cysteine-rich protein with kazal motifs	0.062	3.54E-02	↓
M0R7T1	Phosphatase and actin regulator 4	0.066	1.38E-02	↓
D4ACM8	Frizzled class receptor 7	0.070	3.97E-02	↓
Q68HB8	Protocadherin 7	0.072	4.34E-02	↓

P32736	Opioid-binding protein/cell adhesion molecule	0.073	4.90E-02	↓
P06399	Fibrinogen alpha chain [Cleaved into: Fibrinopeptide A; Fibrinogen alpha chain]	0.077	2.83E-02	↓
A0A0G2JXG3	Cell cycle control protein	0.084	4.05E-02	↓
A0A0G2JY19	Hepatocyte growth factor receptor	0.098	1.78E-02	↓
Q499S6	Cathepsin F	0.142	2.35E-02	↓
A0A0G2JXP0	deleted	0.146	1.89E-02	↓
P13803	Electron transfer flavoprotein subunit alpha, mitochondrial	0.168	2.84E-02	↓
P02680	Fibrinogen gamma chain	0.170	2.96E-02	↓
G3V8N9	Testis expressed 101	0.225	2.27E-02	↓
A0A0G2JXY4	Carbonic anhydrase 15	0.262	1.18E-02	↓
A0A0G2K994	V-set and immunoglobulin domain containing 10	0.283	2.07E-02	↓
Q8R2H2	Integrin beta-3	0.283	3.88E-02	↓
Q9QYL8	Acyl-protein thioesterase 2	0.285	7.95E-03	↓
Q6AYK3	Inositol-3-phosphate synthase 1	0.327	2.30E-02	↓
P25236	Selenoprotein P	0.346	3.66E-03	↓
Q9JIK1	Cadherin-related family member 5	0.365	4.87E-02	↓
A0A0G2JXZ9	protein-tyrosine-phosphatase	0.379	4.83E-02	↓
P34058	Heat shock protein HSP 90-beta	0.405	3.25E-04	↓
B1WBS5	Sodium/mannose cotransporter SLC5A10	0.453	4.40E-02	↓
A0A0G2K980	Ig-like domain-containing protein	1.661	3.07E-02	↑
M0R7Q2	Ig-like domain-containing protein	1.693	3.52E-02	↑
M0RC20	deleted	1.873	2.15E-02	↑
P61972	Nuclear transport factor 2	1.986	1.27E-02	↑
D3ZJF9	Alpha-galactosidase	2.055	1.70E-02	↑
A0A0G2JXI1	Ac2-120	2.057	1.11E-02	↑
P47967	Galectin-5	2.145	1.92E-02	↑
Z4YNX7	Cystatin-related protein 2	2.149	2.02E-02	↑
P10758	Lithostathine	2.235	3.29E-02	↑

Q5I0E1	Leucine-rich alpha-2-glycoprotein 1	2.333	1.41E-03	↑
M0R7M5	deleted	2.410	3.83E-02	↑
P70490	Lactadherin	2.753	3.89E-02	↑
A0A0G2K3W2	Coagulation factor V	2.791	2.80E-02	↑
A0A140TAI2	Biotinidase	2.842	8.33E-03	↑
Q80ZA3	Serine peptidase inhibitor, clade F, member 1	3.127	1.30E-02	↑
Q6AXR4	Beta-hexosaminidase subunit beta	3.177	1.46E-02	↑
A0A0H2UHH2	Amyloid P component, serum	3.260	2.58E-02	↑
P30152	Neutrophil gelatinase-associated lipocalin	3.267	1.91E-02	↑
Q00657	Chondroitin sulfate proteoglycan 4	3.297	2.06E-02	↑
Q5XI77	Annexin	3.346	8.95E-03	↑
M0RDA4	receptor protein-tyrosine kinase	3.503	1.40E-02	↑
A0A0G2JY48	receptor protein-tyrosine kinase	3.504	5.89E-03	↑
A0A0G2K5X3	deleted	3.533	3.88E-02	↑
Q641X3	Beta-hexosaminidase subunit alpha	3.549	4.40E-02	↑
Q9QZK9	Deoxyribonuclease-2-beta	3.555	4.08E-02	↑
Q920A6	Retinoid-inducible serine carboxypeptidase	3.638	4.99E-03	↑
D4A4R7	Serpin family A member 1F	3.757	1.76E-02	↑
F1MA98	Nucleoprotein TPR	4.262	3.22E-02	↑
P45479	Palmitoyl-protein thioesterase 1	4.525	3.34E-02	↑
Q5I0D5	Phospholysine phosphohistidine inorganic pyrophosphate phosphatase	4.774	2.79E-02	↑
G3V7D0	Matrix metallopeptidase 8	4.890	1.98E-02	↑
A0A0G2JZN1	deleted	5.142	4.03E-02	↑
Q32KK2	Arylsulfatase A	5.412	2.33E-02	↑
G3V862	Angiopoietin-like 2	5.826	3.90E-02	↑
Q9Z2Y9	Klotho	6.035	1.23E-02	↑
Q32KJ6	N-acetylgalactosamine-6-sulfatase	6.364	3.41E-02	↑
B2RYC9	Glucosylceramidase	6.461	5.14E-03	↑

Q80WD1	Reticulon-4 receptor-like 2	6.905	4.90E-02	↑
Q6P7S1	Acid ceramidase	7.057	2.43E-02	↑
D3ZY02	Protein-glucosylgalactosylhydroxylysine glucosidase	7.293	2.83E-02	↑
F1MAN8	Laminin subunit alpha 5	7.979	4.31E-02	↑
Q66HT5	CCN family member 1	9.008	3.96E-02	↑
Q6P762	Alpha-mannosidase	9.213	2.90E-02	↑
D4ACR1	RCG64219-like	9.576	2.19E-02	↑
D4AE30	Prostate and testis expressed C	9.649	4.20E-02	↑
F1LXY6	deleted	11.107	1.46E-02	↑
F1M091	Kallikrein m	11.174	3.48E-02	↑
A0A0G2K8F6	Alpha-mannosidase	11.469	2.22E-03	↑
G3V8X9	Serine peptidase inhibitor	13.180	4.40E-02	↑
Q5FVH2	5'-3' exonuclease PLD3	15.910	3.46E-02	↑
F1LWD0	Ig-like domain-containing protein	25.353	4.22E-02	↑
A0A0G2K680	Serine peptidase inhibitor, Kunitz type, 3	43.172	4.78E-02	↑

3.2.6.2 差异蛋白功能分析

将鉴定到的差异蛋白于 Pubmed 数据库进行文献检索。

在菜籽油组下调的差异蛋白中，共有 20 个差异蛋白下调幅度最大、变化为“从有到无”，已有文献证明其中有多个蛋白质与免疫炎症、氧化应激等有关：Thrombospondin 4 (FC=0, P= 4.46E-02)是一种应激诱导型分泌糖蛋白，在组织损伤和愈合中具有关键作用，在心脏和骨骼肌中可激活适应性内质网应激反应并增强肌膜稳定性；Thrombospondin 4 通过分泌途径的缺陷通量会损害心肌细胞膜的稳定性并导致心肌病[44]。Interleukin 10 receptor subunit beta (FC=0, P= 2.63E-02)是 Interleukin 10 receptor 的组成成分之一，是所有 IL-10 细胞因子家族成员共有的，而白细胞介素-10 是一种 2 型 T 辅助细胞细胞因子，具有广泛的抗炎作用[45][46]。Ring finger protein 150 (FC=0, P= 2.83E-02)可能参与调节神经元中的抗氧化应激信号通路，增强神经元对氧化应激的抵抗能力，从而减少神经元的损伤和死亡[47]。Interleukin 17 receptor A (FC=0, P= 2.50E-02)是白细胞介素-17A 的受体，白细胞介素-17A 是一种促炎细胞因子，与结直肠癌的快速恶性进展和治疗抵抗有关[48]。Endothelial protein C recepto (FC=0, P=

3.81E-02)在正常稳态、抗凝途径、炎症和细胞干性中发挥积极作用，被认为是炎症性疾病的潜在效应器或介质[49]。Cell surface glycoprotein CD200 receptor 1 (CD200R) (FC=0, P= 4.12E-02)的唯一已知功能配体是CD200，它们的相互作用导致CD200R表达细胞的抗炎信号激活，当这种相互作用因衰老或疾病而变得不足时，会发生慢性炎症[50]。此外，Protein O-linked-mannose beta-1,2-N-acetylglucosaminyltransferase 1 (POMGnT1) (FC=0, P= 3.26E-02)主要在神经元中表达，在神经胶质细胞中也有一定程度的表达，POMGnT1在阿尔茨海默病小鼠和细胞模型中的表达下降[51]。

在上调的差异蛋白中，Serine peptidase inhibitor Kunitz type 3 (FC=43.172 P= 4.78E-02)是变化倍数最大的，它参与了血液凝固和纤溶、肿瘤免疫、炎症调节以及抵抗细菌和真菌感染等过程[52]。CCN family member 1 (FC=9.008, P= 3.96E-02)是一种细胞外基质蛋白，在伤口愈合过程中具有潜在作用，通过促进角质形成细胞迁移和增殖加速再上皮化[53]。

3.2.6.3 差异蛋白富集生物学过程分析

使用DAVID数据库对成组分析鉴定到的105个差异蛋白进行生物学过程（Biological process, BP）富集分析。结果显示，共有51个BP通路被显著富集（$P<0.05$），详细信息列于图6。

与其他食用油组相比，菜籽油组富集到的通路含有大量与免疫相关的通路，包括Fc-γ受体信号通路、免疫球蛋白介导的免疫反应、细胞对白细胞介素6的反应、免疫反应的调节、内皮细胞增殖的正调节、内皮细胞凋亡过程的负调控、抗体依赖性细胞毒性、内皮细胞迁移的正调控。有研究发现，菜籽油在支持断奶小鼠的获得性免疫能力方面表现出一定的积极作用，尤其是在促进抗体反应方面[54]。

此外，还富集到了很多代谢过程相关的通路，如脂质储存、寡糖分解代谢过程、碳水化合物代谢过程等。值得注意的是“细胞对β淀粉样蛋白的反应”通路，大脑中的淀粉样蛋白β聚集体在阿尔茨海默病的发病机制中起着核心作用，而有研究表明食用植物油可以作为预防或辅助策略以减缓或阻止神经退行性疾病的进展[55][56]。

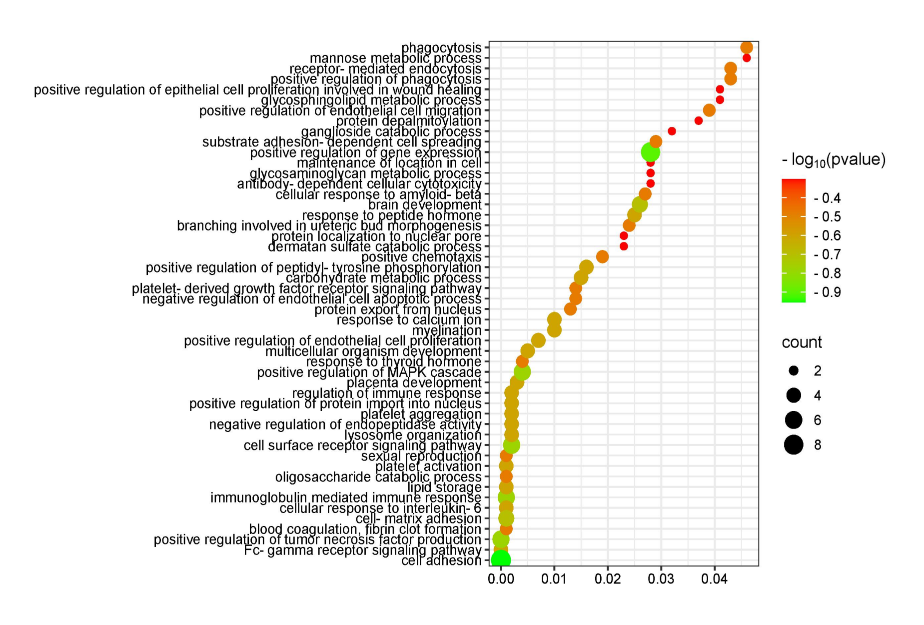


图 6 菜籽油组与对照组差异蛋白富集到的生物学过程

3.2.7 不同食用油成组分析共有差异蛋白

统计五组实验共有的差异蛋白，发现共有的差异蛋白较少，说明不同的食用油对机体的影响是不同的。但其中有两种蛋白 Amyloid P component serum、5'-3' exonuclease PLD3 在所有实验组尿液中均上调。Amyloid P component serum 被认为可能通过与 β -淀粉样蛋白结合增加其稳定性以及诱导神经元凋亡等方式促进包括阿尔茨海默病在内的神经退行性疾病的进展[57]。5'-3' exonuclease PLD3 在大脑神经元中高度表达，在阿尔茨海默病患者大脑中水平下调，且与淀粉样前体蛋白和淀粉样β蛋白水平呈负相关，PLD3 可能通过淀粉样前体蛋白处理来参与阿尔茨海默病的发病机制[58]。

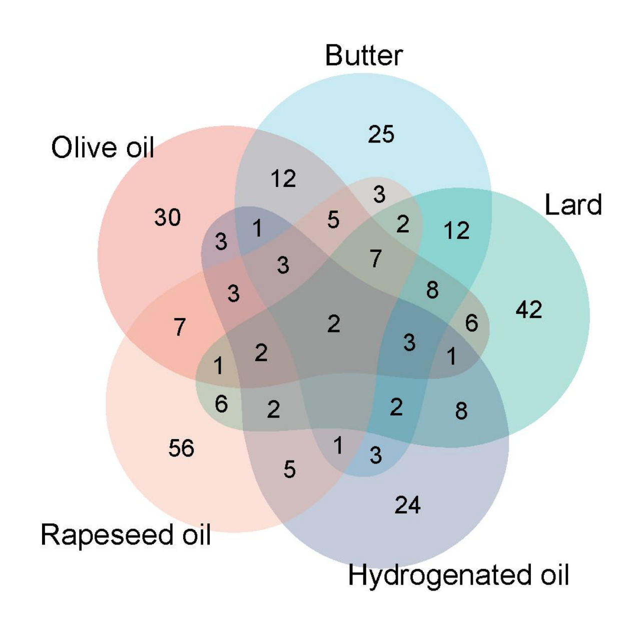


图 7 橄榄油组、黄油组、猪油组、氢化植物油组、菜籽油组尿蛋白质组共有差异蛋白

3.3 尿液翻译后修饰成组分析

3.3.1 随机分组

将对照组样品（n=5）和实验组样品（n=5）随机分成两组，共有 126 种分组。在所有随机组合类型中，按照相同的筛选条件计算所有随机次数的翻译后修饰平均数。翻译后修饰平均数与正常分组下得到的翻译后修饰的比值即为随机产生的翻译后修饰比例，列于表 8。这些结果表明，随机生成的翻译后修饰占比较大，说明短期摄入不同食用油对大鼠机体内的翻译后修饰影响较小。

表 8 随机分组得到的随机产生差异修饰比例

对照组-实验组	A-B	A-C	A-D	A-E	A-F
随机产生蛋白比例	72.1%	72.6%	48.5%	83.0%	20.4%

3.3.2 橄榄油组翻译后修饰成组分析

将橄榄油组与对照组翻译后修饰进行比较，筛选差异修饰条件为：FC≥ 1.5 或≤0.67，双尾配对 t 检验 P<0.05。结果表明，相对于对照组，橄榄油组共鉴定到 41 个差异修饰，其中 17 种下调，24 种上调。将差异蛋白按 FC 由小到大的顺序排列，详细信息列于表 9。

在产生了上调/下调 10 倍以上差异修饰的蛋白质中： P97574 即 Stanniocalcin-1（FC=0，P= 4.59E-02），可能参与那些具有活跃消化和吸收功能的部位的胃肠道和肾脏的消化和吸

收[59]。

表 9 橄榄油组与对照组以 FC≥1.5 或≤0.67，P<0.05 筛选的尿蛋白质组差异修饰

Uniprot ID	Peptide	Modification	A 组	B 组	Flod change	P value
P02761	EKIEENGSMRVFMQHIDVLENSLGFK	0,GIST-Quat[AnyN-term];	2.4	0.0	0.000	4.18E-02
P02761	IDVLENSLGFK	1,Dioxidation[I];	1.0	0.0	0.000	3.41E-02
P0DP29	DGNGYISAAELR	3,Deamidated[N];	4.2	0.0	0.000	4.54E-02
P0DP30	DGNGYISAAELR	3,Deamidated[N];	4.2	0.0	0.000	4.54E-02
P0DP31	DGNGYISAAELR	3,Deamidated[N];	4.2	0.0	0.000	4.54E-02
P14046	KQSGVKEEHSFTVMEFVLPR	0,SPITC_13C(6)[AnyN-term];	2.0	0.0	0.000	4.74E-02
P36373	NNLLEDEPFAQHR	3,Xle->Gln[L];	1.4	0.0	0.000	2.49E-02
P36374	NNLLEDEPFAQHR	3,Xle->Gln[L];	1.4	0.0	0.000	2.49E-02
P97574	MIAEVQEDCYSK	9,Carbamidomethyl[C];	9.0	0.0	0.000	4.59E-02
Q03626	KQSGVKEEHSFTVMEFVLPR	0,SPITC_13C(6)[AnyN-term];	2.0	0.0	0.000	4.74E-02
Q6IE52	KQSGVKEEHSFTVMEFVLPR	0,SPITC_13C(6)[AnyN-term];	2.0	0.0	0.000	4.74E-02
Q9JJ19	IVEVNGVCMEGK	8,Carbamidomethyl[C];9,Oxidation[M];	4.8	0.0	0.000	3.05E-02
Q9JJ19	IVEVNGVCMEGK	8,Carbamidomethyl[C];	6.6	0.6	0.091	4.44E-02
P15083	SSVTFECDLGR	7,Carbamidomethyl[C];	52.8	11.2	0.212	3.28E-02
P81828	LALQCFRCTSFDSTGFCHVGR	5,Carbamidomethyl[C];17,Carbamidomethyl[C];	1.6	0.4	0.250	3.27E-02
P83121	HICQTYPDEICAWVVVTTR	3,NEM_2H(5)[C];	118.4	35.0	0.296	4.72E-02
P26644	ITCPPPPIPK	3,Carbamidomethyl[C];	27.8	13.6	0.489	3.10E-02
P02625	SMTDLLSAEDIKK	0,Acetyl[ProteinN-term];	3.6	7.2	2.000	3.67E-02
Q64240	ECLQTCR	2,Carbamidomethyl[C];6,Carbamidomethyl[C];	6.8	14.4	2.118	3.40E-02
P07522	TTTYAAAGPPR	1,Dimethylphosphothione[T];	1.6	3.4	2.125	8.58E-03
P22282	LDNCPFEEQTEQLKR	4,Carbamidomethyl[C];	70.4	149.6	2.125	3.04E-02

P14841	PQEADASEEGVQR	1,Pro->Cys[P];	0.6	1.4	2.333	1.61E-02
Q64240	QGPCRAFAELWAFDAAQGK	4,BHT[C];	8.8	21.6	2.455	4.04E-02
P01835	GVLDSVTDQDSK	0,glycidamide[AnyN-term];	7.0	18.2	2.600	2.49E-02
P01836	GVLDSVTDQDSK	0,glycidamide[AnyN-term];	7.0	18.2	2.600	2.49E-02
P27590	CPHTEDTTIQVTENGESSQAR	1,Carbamidomethyl[C];14,Deamidated[N];	1.0	2.6	2.600	3.49E-02
P20767	NSFTCQVTHEGNTVEK	1,Deamidated[N];5,Carbamidomethyl[C];	4.0	14.4	3.600	3.05E-02
P01835	DSTYSMSSTLSLTK	6,Carbamidomethyl[M];	2.2	9.0	4.091	1.56E-04
P01836	DSTYSMSSTLSLTK	6,Carbamidomethyl[M];	2.2	9.0	4.091	1.56E-04
P98158	CQTTNICVPR	1,Carbamidomethyl[C];7,Carbamidomethyl[C];	1.0	4.6	4.600	3.27E-02
Q64230	PVENRQAIMTILDQEPDAR	0,SPITC_13C(6)[AnyN-term];	1.0	4.6	4.600	6.05E-03
P22282	LDNCPFEEQTEQLKR	3,Deamidated[N];4,Carbamidomethyl[C];	0.6	2.8	4.667	4.02E-02
P01835	RDGVLDSVTDQDSK	13,Formyl[S](Ser->Asp[S]);	1.6	7.6	4.750	1.67E-02
P01836	RDGVLDSVTDQDSK	13,Formyl[S](Ser->Asp[S]);	1.6	7.6	4.750	1.67E-02
P22282	LDNCPFEEQTEQLKR	4,CarbamidomethylDTT[C];	2.0	10.4	5.200	2.77E-02
Q68FP1	PKAGALNSNDAFVLK	0,Unknown_420[AnyN-term];	1.0	5.8	5.800	3.27E-02
P01835	RDGVLDSVTDQDSK	13,Carbonyl[S];	0.6	6.0	10.000	8.58E-03
P01836	RDGVLDSVTDQDSK	13,Carbonyl[S];	0.6	6.0	10.000	8.58E-03
Q6P7A9	AVPTQCDVTPNSR	6,Carbamidomethyl[C];	0.6	8.4	14.000	4.46E-04
Q63041	QDLNDNDAYSVFQSIGLK	0,Propionyl_13C(3)[AnyN-term];	0.2	3.0	15.000	1.89E-02
P22057	GHDTVQPNFQQDK	4,Thiophospho[T];	0.6	9.2	15.333	2.62E-03

3.3.3 黄油组翻译后修饰成组分析

将黄油组与对照组翻译后修饰进行比较，筛选差异修饰条件为：FC≥ 1.5 或≤0.67，双尾配对 t 检验 P<0.05。结果表明，相对于对照组，黄油组共鉴定到 49 个差异修饰，其中 4 种

下调，45 种上调。将差异蛋白按 FC 由小到大的顺序排列，详细信息列于表 10。

在产生了上调/下调 10 倍以上的差异修饰的蛋白质中：P02770 即 Albumin（FC=37,P= 1.87E-02），在运输各种内源性和外源性分子以及维持血液的胶体渗透压方面起着至关重要的作用，具有许多酶活性，其游离的硫醇基团决定了该蛋白质可以参与氧化还原反应[60]。Q5FVF9 即 Biotinidase（FC=24，P= 4.78E-02），是一种帮助身体重复使用和回收食物中生物素的酶[61]。

表 10 黄油组与对照组以 FC≥1.5 或≤0.67，P<0.05 筛选的尿蛋白质组差异修饰

Uniprot ID	Peptide	Modification	A 组	C 组	Flod change	P value
P30919	YCGPYKPPDFLEQNNR	2,Carbamidomethyl[C];	3.8	0.8	0.211	3.41E-02
P02780	SGCSILDEVIR	3,CarbamidomethylDTT[C];	1.4	0.4	0.286	3.41E-02
Q9JHB9	SGCSILDEVIR	3,CarbamidomethylDTT[C];	1.4	0.4	0.286	3.41E-02
Q62740	GYSVPTAACR	9,Carbamidomethyl[C];	16.2	7.6	0.469	1.41E-02
P01836	TSSSPVVKSFNR	8,Carbamyl[K];	15.0	24.6	1.640	4.47E-02
P01835	TSSSPVVKSFNR	8,Carbamyl[K];	15.0	24.6	1.640	4.47E-02
P22282	LDNCPFEEQTEQLKR	4,Carbamidomethyl[C];	70.4	128.6	1.827	6.48E-03
P20767	LTVFPPSTEELQGNK	2,Hex(1)Pent(2)[T];	13.6	27.2	2.000	3.35E-02
P20767	NSFTCQVTHEGNTVEK	5,Carbamidomethyl[C];	26.4	54.0	2.045	7.97E-03
P22282	LDNCPFEEQTEQLK	4,Carbamidomethyl[C];	66.8	138.2	2.069	2.52E-03
P20611	FPLGPCPR	6,Carbamidomethyl[C];	9.2	19.2	2.087	3.36E-02
P07522	CHELVACPGNR	1,Carbamidomethyl[C];7,Carbamidomethyl[C];	2.2	5.2	2.364	2.31E-02
P07522	RITEGVDTPEGLAVDWIGR	2,Xle->Asn[I];	1.2	3.2	2.667	2.17E-02
P29598	TDSCSGDSGGPLICNIDGR	4,Carbamidomethyl[C];14,Carbamidomethyl[C];	5.4	15.4	2.852	1.59E-02
P42854	SSGNSGQNVWIGLHDPTLGQEPNR	4,Deamidated[N];8,Deamidated[N];	1.0	3.0	3.000	2.17E-02
P20767	TLTVFPPSTEELQGNK	1,Hex(2)[T];	2.8	9.6	3.429	1.30E-02
P02761	WFSIVVASNK	3,Hex(1)Pent(2)[S];	3.0	10.6	3.533	4.40E-02

P09006	SMEEILEGLK	0,Biotin[AnyN-term];	1.6	6.0	3.750	4.85E-02
P07522	VNLDPASVPPR	2,Asn->Cys[N];	4.8	19.0	3.958	4.30E-02
P20767	NSFTCQVTHEGNTVEK	1,Deamidated[N];5,Carbamidomethyl[C];	4.0	16.0	4.000	1.86E-02
P42854	IGLHDPTLGQEPNR	4,His->Xle[H];	0.4	1.6	4.000	3.27E-02
P42854	WRENNCISELPYVCK	4,Deamidated[N];6,Carbamidomethyl[C];14,Carbamidomethyl[C];	4.8	19.4	4.042	3.64E-02
P01836	DSTYSMSSTLSLTK	6,Carbamidomethyl[M];	2.2	9.8	4.455	3.26E-03
P01835	DSTYSMSSTLSLTK	6,Carbamidomethyl[M];	2.2	9.8	4.455	3.26E-03
P20767	FPPSTEELQGNK	0,Formyl[AnyN-term];	0.8	4.0	5.000	4.01E-02
P22282	EICYFVVYPDYIEQNIHAVR	0,Amidine[AnyN-term];	0.2	1.0	5.000	1.61E-02
P36373	KPGDDHSNDLMLLHLSQPADITDGVK	5,Cation_Fe[III][D];	0.4	2.0	5.000	3.49E-02
P01835	DYESHNLYTCEVVHKTSSSPVVK	10,Ub-VME[C];	0.4	2.4	6.000	4.74E-02
P02767	FASGKTAESGELHGLTTDEK	6,PhosphoHexNAc[T];	0.4	2.4	6.000	4.74E-02
Q4FZV0	FQSAVQYAECQSK	10,Carbamidomethyl[C];	1.0	6.0	6.000	3.83E-02
P07522	PSSLVVVHPLAK	2,Dehydrated[S];	0.4	2.8	7.000	2.40E-02
Q63041	MGASEVAQEVEVR	0,CLIP_TRAQ_2[AnyN-term];	0.4	2.8	7.000	4.18E-02
Q01177	GTPCQEWAAQEPHSHR	4,NEM_2H(5)[C];	0.2	1.4	7.000	3.88E-03
Q9EPB1	SLPFGVQSTQR	0,C+12[AnyN-term];	0.4	2.8	7.000	2.40E-02
P22282	PGETMYYISLPGSVR	0,Phenylisocyanate_2H(5)[AnyN-term];	2.0	14.2	7.100	1.51E-02
P20767	QVTHEGNTVEK	2,Val->Ser[V];	1.8	13.6	7.556	2.62E-02
P02761	LCEAHGITR	2,maleimide[C];	0.6	5.8	9.667	3.67E-02
P01835	ADYESHNLYTCEVVHK	7,Deamidated[N];11,Carbamidomethyl[C];	0.8	7.8	9.750	2.79E-02
Q64240	YCGVPGDGYEELTR	2,Bromobimane[C];	0.4	4.2	10.500	3.40E-02

Q6P7A9	AVPTQCDVTPNSR	6,Carbamidomethyl[C];	0.6	7.4	12.333	2.99E-02
P01836	RDGVLDSVTDQDSK	14,Lys->Asp[K];	0.4	5.2	13.000	3.27E-02
P01835	RDGVLDSVTDQDSK	14,Lys->Asp[K];	0.4	5.2	13.000	3.27E-02
P01836	RDGVLDSVTDQDSK	13,Carbonyl[S];	0.6	8.6	14.333	3.66E-02
P01835	RDGVLDSVTDQDSK	13,Carbonyl[S];	0.6	8.6	14.333	3.66E-02
P22057	GHDTVQPNFQQDK	4,Thiophospho[T];	0.6	10.4	17.333	1.16E-02
Q5FVF9	NLDVYEQQVMAAAQK	1,dHex[N];	0.2	4.8	24.000	4.78E-02
P36375	NNLFEDEPFAQYR	0,Dimethyl_2H(4)[AnyN-term];	0.2	6.0	30.000	3.53E-02
P00689	ALVFVDNHDNQR	6,Cation_Na[D];	0.2	6.0	30.000	3.84E-02
P02770	TVMGDFAQFVDK	3,Met->Lys[M];	0.2	7.4	37.000	1.87E-02

3.3.4 猪油组翻译后修饰成组分析

将猪油组与对照组翻译后修饰进行比较，筛选差异修饰条件为：FC≥ 1.5 或≤0.67，双尾配对 t 检验 P<0.05。结果表明，相对于对照组，猪油组共鉴定到 99 个差异修饰，其中 23 种下调，76 种上调。将差异蛋白按 FC 由小到大的顺序排列，详细信息列于表 11。

在产生了上调/下调 10 倍以上的差异修饰的蛋白质中：P07151 即 Beta-2-microglobulin（FC=15，P= 8.64E-03），在老年人氧化应激状态中可能发挥作用，可以作为氧化应激的新型生物标志物[63]。P11232 即 Thioredoxin （FC=0.091，P= 3.41E-02），在维持细胞的氧化还原状态和调节氧化还原信号传导中起着重要作用，和谷胱甘肽一起在对抗氧化应激中起着核心作用[64]。

表 11 猪油组与对照组以 FC≥1.5 或≤0.67，P<0.05 筛选的尿蛋白质组差异修饰

Uniprot ID	Peptide	Modification	A 组	D 组	Flod change	P value
P02761	EKIEENGSMRVFMQHIDVLENSLGFK	0,GIST-Quat[AnyN-term];	2.4	0.0	0.000	4.18E-02
P02761	IDVLENSLGFK	1,Dioxidation[I];	1.0	0.0	0.000	3.41E-02
P22283	LVNCPFEEQTEQLK	4,dichlorination[C];	1.4	0.0	0.000	2.49E-02
P32038	DVAGWGVVTHAGR	0,mTRAQ_13C(6)15N(2)[Any	2.2	0.0	0.000	2.95E-02

		N-term];				
P36373	NNLLEDEPFAQHR	3,Xle->Gln[L];	1.4	0.0	0.000	2.49E-02
P36374	NNLLEDEPFAQHR	3,Xle->Gln[L];	1.4	0.0	0.000	2.49E-02
Q99PS8	HPPVFGLCR	8,Carbamidomethyl[C];	9.0	0.0	0.000	3.67E-02
Q9JJ19	IVEVNGVCMEGK	8,Carbamidomethyl[C];9,Oxidation[M];	4.8	0.0	0.000	3.05E-02
P30919	YCGPYKPPDFLEQNNR	2,Carbamidomethyl[C];	3.8	0.2	0.053	4.91E-02
P11232	AFQEALAAAGDK	0,Pyridylacetyl[AnyN-term](Phenylisocyanate[AnyN-term]);	2.2	0.2	0.091	3.41E-02
P02761	IDVLENSLGFK	2,Cation_Ca[II][D];	4.0	0.4	0.100	3.27E-02
P02761	LNGDWFSIVVASNK	4,Cation_Al[III][D];	8.6	1.0	0.116	4.78E-02
P42854	SGQNVWIGLHDPTLGQEPNR	1,HexNAc(1)dHex(1)[S];	10.2	1.2	0.118	3.35E-02
P00787	HCGIESEIVAGIPR	2,Cytopiloyne[C];	8.0	1.0	0.125	4.94E-02
P20059	GECQSEGVLFFQGNR	3,Amidino[C];	1.6	0.2	0.125	2.49E-02
P02780	SGSGCSILDEVIR	5,Malonyl[C];	2.4	0.4	0.167	3.41E-02
Q9JHB9	SGSGCSILDEVIR	5,Malonyl[C];	2.4	0.4	0.167	3.41E-02
P27590	STDYGAGYSCDSDMHGWYR	10,monomethylphosphothione[C];	2.6	1.0	0.385	3.49E-02
P27590	CPHTEDTTIQVTENGESSQAR	1,CarbamidomethylDTT[C];	6.2	2.8	0.452	3.88E-02
Q62740	GYSVPTAACR	9,Carbamidomethyl[C];	16.2	8.0	0.494	1.55E-03
P81827	ESLDSTGLCR	9,Carbamidomethyl[C];	14.6	8.6	0.589	2.44E-02
P08649	EPFLSCCK	6,Carbamidomethyl[C];7,Carbamidomethyl[C];	12.6	8.2	0.651	2.95E-02
Q62740	ESGDPSTCAFQR	8,Carbamidomethyl[C];	19.8	13.0	0.657	3.64E-03
P02761	EKIEENGSMR	9,Oxidation[M];	85.6	134.8	1.575	3.78E-02
P02780	SGSGCSILDEVIR	5,CarbamidomethylDTT[C];	17.6	28.0	1.591	6.43E-04
Q9JHB9	SGSGCSILDEVIR	5,CarbamidomethylDTT[C];	17.6	28.0	1.591	6.43E-04
P98158	NPCASASCSHLCLLSAQAPR	3,Carbamidomethyl[C];8,Carbamidomethyl[C];12,Carbamido	6.8	11.4	1.676	4.27E-02

		methyl[C];				
P98158	HQCLCEEGYILER	3,Carbamidomethyl[C];5,Carbamidomethyl[C];	18.0	31.6	1.756	1.97E-02
P22283	CSFQWEFCNIK	1,Carbamidomethyl[C];8,Carbamidomethyl[C];	12.8	23.6	1.844	2.96E-02
P10252	EDQGVDYTWYEDSGPFPQR	1,Glu->Xle[E];	2.8	5.2	1.857	9.26E-03
P01835	TSSSPVVKSFNR	8,Carbamyl[K];	15.0	29.2	1.947	3.87E-02
P01836	TSSSPVVKSFNR	8,Carbamyl[K];	15.0	29.2	1.947	3.87E-02
P01835	DGVLDSVTDQDSK	1,Cation_Na[D];	3.6	7.2	2.000	2.88E-02
P01836	DGVLDSVTDQDSK	1,Cation_Na[D];	3.6	7.2	2.000	2.88E-02
P07632	ISLSGEHSIIGR	2,monomethylphosphothione[S];	4.2	8.4	2.000	1.46E-02
P02780	IRGTINSTVTLHDYMK	0,Diethylphosphate[AnyN-term];	8.4	17.6	2.095	8.92E-03
Q9JHB9	IRGTINSTVTLHDYMK	0,Diethylphosphate[AnyN-term];	8.4	17.6	2.095	8.92E-03
P20059	CNADPGLSALLSDHR	0,Pyro-carbamidomethyl[AnyN-termC];	5.2	11.0	2.115	9.49E-03
Q63041	QNNICFDNWWVDEYHTQADHSAAR	5,Carbamidomethyl[C];	5.2	11.4	2.192	3.27E-02
P02780	QCFLDQTDK	0,Gln->pyro-Glu[AnyN-termQ];2,Carbamidomethyl[C];	139.0	305.6	2.199	1.29E-02
P22282	TPGETMYYISLPGSVR	6,Oxidation[M];	7.4	16.6	2.243	2.39E-02
P29598	TDSCSGDSGGPLICNIDGR	4,Carbamidomethyl[C];14,Carbamidomethyl[C];	5.4	12.8	2.370	1.26E-02
P02781	ELEEFDAPPEAVEANLK	6,Asp->Lys[D];	17.8	43.0	2.416	3.37E-03
P02761	VFMQHIDVLENSLGFK	0,Delta_H(2)C(2)[AnyN-term];	7.2	17.6	2.444	1.65E-02
P02761	CEAHGITR	1,Glutathione[C];	11.6	28.4	2.448	1.46E-02
P02780	ASGSGCSILDEVIR	6,SulfurDioxide[C];	5.0	12.4	2.480	2.13E-02

Q9JHB9	ASGSGCSILDEVIR	6,SulfurDioxide[C];	5.0	12.4	2.480	2.13E-02
P20767	NSFTCQVTHEGNTVEK	1,Deamidated[N];5,Carbamidomethyl[C];	4.0	10.2	2.550	5.10E-03
P22282	LDNCPFEEQTEQLK	4,Carbamidomethyl[C];	66.8	177.2	2.653	5.66E-03
P00758	HLSQPADITDGVK	4,Gln->Phe[Q];	0.6	1.6	2.667	3.41E-02
P07647	LVSQSFQHPDYIPVFMR	16,Oxidation[M];	1.8	4.8	2.667	2.85E-02
P36373	HLSQPADITDGVK	4,Gln->Phe[Q];	0.6	1.6	2.667	3.41E-02
P01835	DSTYSMSSTLSLTK	6,Carbamidomethyl[M];	2.2	6.2	2.818	3.09E-02
P01836	DSTYSMSSTLSLTK	6,Carbamidomethyl[M];	2.2	6.2	2.818	3.09E-02
P22057	QGHDTVQPNFQQDK	0,Gln->pyro-Glu[AnyN-termQ];	1.2	3.4	2.833	4.18E-03
P98158	GRTCKVTGSENPLLVVASR	0,3sulfo[AnyN-term];	1.2	3.4	2.833	2.95E-02
P07647	AYDHNNDLMLLHLSK	6,Deamidated[N];	6.2	17.6	2.839	3.98E-03
P22282	LDNCPFEEQTEQLKR	4,Carbamidomethyl[C];	70.4	205.6	2.920	4.71E-02
P02761	VFMQHIDVLENSLGFK	12,Formyl[S](Ser->Asp[S]);	5.8	18.4	3.172	1.99E-02
P06760	YRQPLRESGPTLDMPVPSSFNDITQEAELR	7,Cation_Ni[II][E];	0.8	2.6	3.250	3.67E-02
P22282	TPGETMYYISLPGSVR	4,Cation_Na[E];	23.6	77.0	3.263	6.76E-03
P02761	ETFQLMVLYGR	0,Diisopropylphosphate[AnyN-term];	1.4	4.8	3.429	4.34E-02
P42854	SSGNSGQNVWIGLHDPTLGQEPNR	4,Deamidated_18O(1)[N](Delta_H(1)N(-1)18O(1)[N]);	7.0	24.4	3.486	1.91E-02
P01835	VLDSVTDQDSK	0,mTRAQ_13C(6)15N(2)[AnyN-term];	1.6	5.8	3.625	2.77E-02
P01836	VLDSVTDQDSK	0,mTRAQ_13C(6)15N(2)[AnyN-term];	1.6	5.8	3.625	2.77E-02
P29598	KPSSTVDQQGFQCGQK	13,Carbamidomethyl[C];	3.8	14.8	3.895	3.07E-02
P02782	EMYNAPPAAVEAK	0,Unknown_250[AnyN-term];	2.2	8.8	4.000	1.00E-02
P14562	CNSEEHIFVSK	1,Carbamidomethyl[C];	0.4	1.6	4.000	3.88E-03

P36373	NLLEDEPFAQHR	0,dNIC[AnyN-term];	1.8	7.6	4.222	6.48E-03
P36374	NLLEDEPFAQHR	0,dNIC[AnyN-term];	1.8	7.6	4.222	6.48E-03
P98158	SSDSFSAASVIFSNGR	0,C+12[AnyN-term];	0.6	2.6	4.333	3.41E-02
P02761	GETFQLMVLYGR	0,C+12[AnyN-term];	1.2	5.4	4.500	1.71E-02
P02761	VFMQHIDVLENSLGFK	7,Propargylamine[D];	9.0	41.4	4.600	3.49E-02
P02781	ELEEFDAPPEAVEANLK	0,Methyl[AnyN-term];	0.6	2.8	4.667	4.02E-02
P60711	EHPVLLTEAPLNPK	7,Hex(2)Sulf(1)[T];	0.6	2.8	4.667	1.09E-02
P63259	EHPVLLTEAPLNPK	7,Hex(2)Sulf(1)[T];	0.6	2.8	4.667	1.09E-02
P15684	MLSSFLTEDLFK	1,Met->Aha[M];	0.2	1.0	5.000	1.61E-02
P02761	MQHIDVLENSLGFK	0,SPITC_13C(6)[AnyN-term];	2.4	14.4	6.000	3.88E-03
P07647	AYDHNNDLMLLHLSK	5,Deamidated_18O(1)[N](Delta_H(1)N(-1)18O(1)[N]);	1.4	8.4	6.000	3.73E-02
P30919	PSYQAVEYMR	1,Pro->Cys[P];	0.4	2.6	6.500	2.95E-02
Q4FZV0	FQSAVQYAECQSK	10,Carbamidomethyl[C];	1.0	6.8	6.800	8.42E-06
P01048	GTKKDGAETLYSFK	3,Phosphoadenosine[K];	0.2	1.4	7.000	3.27E-02
P02761	LNGDWFSIVVASNK	12,Formyl[S](Ser->Asp[S]);	0.6	4.2	7.000	3.27E-02
P08932	GTKKDGAETLYSFK	3,Phosphoadenosine[K];	0.2	1.4	7.000	3.27E-02
P32038	LCDVAGWGVVTHAGR	2,Nmethylmaleimide[C];	0.2	1.4	7.000	3.27E-02
P42854	IGLHDPTLGQEPNR	4,His->Xle[H];	0.4	2.8	7.000	4.18E-02
P22282	PGETMYYISLPGSVR	0,Phenylisocyanate_2H(5)[AnyN-term];	2.0	14.4	7.200	4.58E-02
P82450	TFEISCCSDHQCK	6,Carbamidomethyl[C];7,Carbamidomethyl[C];12,Carbamidomethyl[C];	0.2	1.6	8.000	2.49E-02
P07647	AYDHNNDLMLLHLSK	5,Deamidated[N];	2.4	19.6	8.167	2.39E-02
P22282	EICYFVVYPDYIEQNIHAVR	0,Amidine[AnyN-term];	0.2	1.8	9.000	3.49E-02
P81828	QCFRCTSFDSTGFCHVGR	5,Carbamidomethyl[C];14,Carbamidomethyl[C];	1.0	9.4	9.400	9.64E-03
Q64230	PVENRQAIMTILDQEPDAR	0,SPITC_13C(6)[AnyN-term];	1.0	10.2	10.200	2.86E-02

P02770	PPACYGTVLAEFQPLVEEPK	4,Carbamidomethyl[C];	0.2	2.2	11.000	4.74E-02
P22282	LDNCPFEEQTEQLKR	3,Deamidated[N];4,Carbamidomethyl[C];	0.6	7.2	12.000	3.65E-02
Q63041	MGASEVAQEVEVR	0,CLIP_TRAQ_2[AnyN-term];	0.4	5.6	14.000	2.89E-03
P07151	PNIEMSDLSFSK	2,Tris[N];	0.2	3.0	15.000	8.64E-03
P02650	NTMLGQSTEELR	2,Pent(1)HexNAc(1)[T];	0.2	3.2	16.000	9.01E-03
P22282	EICYFVVYPDYIEQNIHAVR	5,Phe->Trp[F];	0.2	4.4	22.000	2.22E-02
P36375	NNLFEDEPFAQYR	0,Dimethyl_2H(4)[AnyN-term];	0.2	5.2	26.000	4.47E-02

3.3.5 氢化植物油组翻译后修饰成组分析

将氢化植物油组与对照组翻译后修饰进行比较，筛选差异修饰条件为：FC≥ 1.5 或≤0.67，双尾配对 t 检验 P<0.05。结果表明，相对于对照组，氢化植物油组共鉴定到 50 个差异修饰，其中 38 种下调，12 种上调。将差异蛋白按 FC 由小到大的顺序排列，详细信息列于表 12。

在发生了上调/下调 10 倍以上差异修饰的蛋白质中：P27590 即 Uromodulin（FC=0.053，P=4.91E-02），在肾脏生理、肾小管运输和矿物质代谢中具有多种功能，较高的血清 Uromodulin 浓度与较高的肾功能和保留的肾储备相关，也与较低的心血管疾病和糖尿病风险相关[65]。

表 12 氢化植物油组与对照组以 FC≥1.5 或≤0.67，P<0.05 筛选的尿蛋白质组差异修饰

Uniprot ID	Peptide	Modification	A 组	E 组	Flod change	P value
P02761	IDVLENSLGFK	1,Dioxidation[I];	1.0	0.0	0.000	3.41E-02
P04937	TNIGPDTMRVTWAPPPSIELTNLLVR	9,Arg->His[R];	1.0	0.0	0.000	3.41E-02
P36373	NNLLEDEPFAQHR	3,Xle->Gln[L];	1.4	0.0	0.000	2.49E-02
P36374	NNLLEDEPFAQHR	3,Xle->Gln[L];	1.4	0.0	0.000	2.49E-02
P60711	MCKAGFAGDDAPR	2,Nmethylmaleimide[C];	0.8	0.0	0.000	1.61E-02
P63259	MCKAGFAGDDAPR	2,Nmethylmaleimide[C];	0.8	0.0	0.000	1.61E-02

Q63621	CDDWGLDTMR	1,Carbamidomethyl[C];	3.8	0.0	0.000	3.04E-02
Q9JJ19	IVEVNGVCMEGK	8,Carbamidomethyl[C];9,Oxidation[M];	4.8	0.0	0.000	3.05E-02
P97574	MIAEVQEDCYSK	9,Carbamidomethyl[C];	9.0	0.0	0.000	4.59E-02
P14046	YMVLVPSQLYTETPEK	2,Oxidation[M];	9.6	0.4	0.042	4.59E-02
Q03626	YMVLVPSQLYTETPEK	2,Oxidation[M];	9.6	0.4	0.042	4.59E-02
Q6IE52	YMVLVPSQLYTETPEK	2,Oxidation[M];	9.6	0.4	0.042	4.59E-02
P27590	AHWSDHCCLWSTEIQVK	4,Hex(1)NeuGc(1)[S];	3.8	0.2	0.053	4.91E-02
P02761	EKIEENGSMRVFMQHIDVLENSLGFK	0,GIST-Quat[AnyN-term];	2.4	0.2	0.083	4.02E-02
P26644	AVFGCHETYK	5,Carbamidomethyl[C];	14.6	1.6	0.110	3.14E-02
P08426	IIRHPSYNANTFDNDIMLIK	7,Tyr->Ala[Y];	6.6	0.8	0.121	1.66E-02
Q9JJ19	IVEVNGVCMEGK	8,Carbamidomethyl[C];	6.6	0.8	0.121	3.37E-02
P02770	LPCVEDYLSAILNR	3,CarbamidomethylDTT[C];	1.6	0.2	0.125	2.49E-02
P01048	LESGNQFVLYR	3,Hex(1)NeuGc(1)[S];	4.8	0.6	0.125	4.24E-02
P01048	DGAETLYSFK	1,Cation_Li[D];	5.0	1.0	0.200	3.74E-02
P08932	DGAETLYSFK	1,Cation_Li[D];	5.0	1.0	0.200	3.74E-02
P26644	ITCPPPPIPK	3,Carbamidomethyl[C];	27.8	5.8	0.209	1.17E-03
P83121	DEICAWVVVTTR	4,Carbamidomethyl[C];	1.8	0.4	0.222	2.49E-02
P81828	DEICAWVVVTTR	4,Carbamidomethyl[C];	1.8	0.4	0.222	2.49E-02
P81827	DEICAWVVVTTR	4,Carbamidomethyl[C];	1.8	0.4	0.222	2.49E-02
P24090	IAATDCTGQEVTDPAK	0,Galactosyl[AnyN-term];	3.0	0.8	0.267	4.02E-02
P07632	ASGEPVVVSGQITGLTEGEHGFHVHQYGDNTQGCTTAGPHFNPH	34,Carbamidomethyl[C];	4.6	1.4	0.304	2.99E-02
P20059	GECQSEGVLFFQGNR	0,Acetyl_2H(3)[AnyN-term];	9.6	3.6	0.375	2.17E-02
P02780	ASGSGCSILDEVIR	6,SulfurDioxide[C];	5.0	2.2	0.440	2.49E-02
Q9JHB9	ASGSGCSILDEVIR	6,SulfurDioxide[C];	5.0	2.2	0.440	2.49E-02
Q62740	GYSVPTAACR	9,Carbamidomethyl[C];	16.2	7.2	0.444	1.27E-02

Q64240	AFAELWAFDAAQGK	9,Cation_Na[D];	2.6	1.2	0.462	2.49E-02
P36373	NNLLEDEPFAQHR	1,Ammonia-loss[N];	2.0	1.0	0.500	3.41E-02
P36374	NNLLEDEPFAQHR	1,Ammonia-loss[N];	2.0	1.0	0.500	3.41E-02
Q01177	CEGETDFICR	1,Carbamidomethyl[C];9,Carbamidomethyl[C];	14.6	7.8	0.534	1.05E-03
P36953	TINPTVDHCCR	9,Carbamidomethyl[C];10,Carbamidomethyl[C];	15.4	8.4	0.545	4.60E-02
P02761	EKIEENGSMR	6,Deamidated[N];	22.0	12.2	0.555	2.69E-02
Q62740	ESGDPSTCAFQR	8,Carbamidomethyl[C];	19.8	13.0	0.657	3.10E-02
P07632	ISLSGEHSIIGR	2,monomethylphosphothione[S];	4.2	9.2	2.190	4.47E-02
P01836	VLDSVTDQDSK	0,mTRAQ_13C(6)15N(2)[AnyN-term];	1.6	4.2	2.625	4.86E-02
P01835	VLDSVTDQDSK	0,mTRAQ_13C(6)15N(2)[AnyN-term];	1.6	4.2	2.625	4.86E-02
P42854	SSGNSGQNVWIGLHDPTLGQEPNR	4,Deamidated_18O(1)[N](Delta_H(1)N(-1)18O(1)[N]);	7.0	20.8	2.971	3.19E-02
P02761	MQHIDVLENSLGFK	0,SPITC_13C(6)[AnyN-term];	2.4	9.0	3.750	2.27E-02
P08426	LGEHNIDVVEGGEQFIDAAKIIRHPSYNANTFDNDIMLIK	20,Carbamyl[K];	0.4	2.4	6.000	4.74E-02
P00758	NLYEDEPFAQHR	3,monomethylphosphothione[Y];	2.8	17.0	6.071	1.52E-02
P01836	RDGVLDSVTDQDSK	7,Formyl[S](Ser->Asp[S]);	0.6	3.8	6.333	2.99E-02
P01835	RDGVLDSVTDQDSK	7,Formyl[S](Ser->Asp[S]);	0.6	3.8	6.333	2.99E-02
P22282	PGETMYYISLPGSVR	0,Phenylisocyanate_2H(5)[AnyN-term];	2.0	13.0	6.500	3.20E-02
P00762	LGEHNINVLEGDEQFINAA	7,Deamidated[N];	0.2	1.4	7.000	3.27E-02
Q9R0T4	DTGVISVVTSGLDR	4,Val->Cys[V];	0.4	3.2	8.000	3.12E-02

3.3.6 菜籽油组翻译后修饰成组分析

将菜籽油组与对照组翻译后修饰进行比较，筛选差异修饰条件为：FC≥ 1.5 或≤0.67，双尾配对 t 检验 P<0.05。结果表明，相对于对照组，菜籽油组共鉴定到 50 个差异修饰，其中 38 种下调，12 种上调。将差异蛋白按 FC 由小到大的顺序排列，详细信息列于表 13。

在发生了上调/下调 10 倍以上差异修饰的蛋白质中：P07632 即 Superoxide dismutase（FC=0，P= 2.95E-02），可以中和超氧自由基并保护生物体免受氧化应激，在抗氧化过程中发挥重要作用[66]。P47853 即 Biglycan（FC=0.045，P= 4.47E-02），可以减少高脂饮食诱导的肥胖，并且可改善小鼠的葡萄糖耐量[67]。

表 13 菜籽油组与对照组以 FC≥1.5 或≤0.67，P<0.05 筛选的尿蛋白质组差异修饰

Uniprot ID	Peptide	Modification	A 组	F 组	Flod change	P value
P02761	FMQHIDVLENSLGFK	0,Phenylisocyanate_2H(5)[AnyN-term];	3.8	0.0	0.000	3.76E-02
P02761	AKLNGDWFSIVVASNK	3,Xle->Ala[L];	5.6	0.0	0.000	4.29E-02
P02761	YVMFHLINFK	8,Deamidated[N];	6.6	0.0	0.000	3.18E-02
P02761	IEENGSMRVFMQHIDVLENSLGFK	6,Dehydrated[S];	0.8	0.0	0.000	1.61E-02
P02761	WFSIVVASNK	0,Hex[AnyN-term];	3.4	0.0	0.000	2.99E-02
P02761	IDVLENSLGFK	1,Dioxidation[I];	1.0	0.0	0.000	3.41E-02
P02770	LPEAQRLPCVEDYLSAILNR	9,CarbamidomethylDTT[C];	1.2	0.0	0.000	3.27E-02
P02770	LPCVEDYLSAILNR	3,CarbamidomethylDTT[C];	1.6	0.0	0.000	3.49E-02
P05544	ITGTKDLYVSQVVHK	0,Carbamyl[AnyN-term];	4.8	0.0	0.000	2.61E-02
P01836	DSTYSMSSTLSLTK	1,Cation_Na[D];	6.8	0.0	0.000	4.00E-02
P01835	DSTYSMSSTLSLTK	1,Cation_Na[D];	6.8	0.0	0.000	4.00E-02
P24090	IAATDCTGQEVTDPAK	0,Galactosyl[AnyN-term];	3.0	0.0	0.000	2.85E-02
P04937	TNIGPDTMRVTWAPPPSIELTNLLVR	9,Arg->His[R];	1.0	0.0	0.000	3.41E-02
P04937	TNIGPDTMRVTWAPPPSIELTNLLVR	2,Deamidated[N];	2.0	0.0	0.000	2.17E-02

P0DP29	DGNGYISAAELR	3,Deamidated[N];	4.2	0.0	0.000	4.54E-02
P0DP30	DGNGYISAAELR	3,Deamidated[N];	4.2	0.0	0.000	4.54E-02
P0DP31	DGNGYISAAELR	3,Deamidated[N];	4.2	0.0	0.000	4.54E-02
P14046	KQSGVKEEHSFTVMEFVLPR	0,SPITC_13C(6)[AnyN-term];	2.0	0.0	0.000	4.74E-02
Q03626	KQSGVKEEHSFTVMEFVLPR	0,SPITC_13C(6)[AnyN-term];	2.0	0.0	0.000	4.74E-02
P05545	QTQGKIAELFSELDER	0,GIST-Quat_2H(3)[AnyN-term];	3.8	0.0	0.000	3.76E-02
P32038	DVAGWGVVTHAGR	0,mTRAQ_13C(6)15N(2)[AnyN-term];	2.2	0.0	0.000	2.95E-02
P32038	QQLTVSIMDR	0,ISD_z+2_ion[AnyN-term];	0.8	0.0	0.000	1.61E-02
Q6IE52	KQSGVKEEHSFTVMEFVLPR	0,SPITC_13C(6)[AnyN-term];	2.0	0.0	0.000	4.74E-02
P08723	LCLTSLSFTTNK	1,Xle->Tyr[L];	1.2	0.0	0.000	3.27E-02
P00758	QPGDDYSNDLMLLHLSQPADITDGVK	4,Cation_Na[D];	1.8	0.0	0.000	3.67E-02
P00758	NLYEDEPFAQHR	0,GIST-Quat[AnyN-term];	5.8	0.0	0.000	3.68E-02
P27590	HTEDTTIQVTENGESSQAR	1,Cresylphosphate[H];	10.4	0.0	0.000	4.51E-02
P27590	STDYGAGYSCDSDMHGWYR	10,Propionamide[C];	2.6	0.0	0.000	4.86E-02
P27590	VCQDPCNVYETLTEYWR	6,4-ONE[C];	2.4	0.0	0.000	4.18E-02
P22282	YIEQNIHAVR	0,ISD_z+2_ion[AnyN-term];	2.0	0.0	0.000	4.74E-02
P07647	VGSICLASGWGMTNPSEMK	5,Carbamidomethyl[C];	3.4	0.0	0.000	2.99E-02
P07632	AVCVLKGDGPVQGVIHFEQK	3,NEMsulfur[C];	2.2	0.0	0.000	2.95E-02
P36373	NNLLEDEPFAQHR	3,Xle->Gln[L];	1.4	0.0	0.000	2.49E-02
P02780	SGSGCSILDEVIR	5,monomethylphosphothione[C];	8.0	0.0	0.000	4.91E-02
P02780	ASGSGCSILDEVIR	0,Acetyl[ProteinN-term];	2.4	0.0	0.000	2.40E-02
Q9JHB9	SGSGCSILDEVIR	5,monomethylphosphothione	8.0	0.0	0.000	4.91E-02

		[C];				
Q9JHB9	ASGSGCSILDEVIR	0,Acetyl[ProteinN-term];	2.4	0.0	0.000	2.40E-02
P01048	QEEGAQELNCNDETVFQAVD TALK	0,Gln->pyro-Glu[AnyN-term Q];10,Carbamidomethyl[C];	3.8	0.0	0.000	2.36E-02
P01048	LESGNQFVLYR	3,Hex(1)NeuGc(1)[S];	4.8	0.0	0.000	3.49E-02
P36374	NNLLEDEPFAQHR	3,Xle->Gln[L];	1.4	0.0	0.000	2.49E-02
P06866	IEDDSCPKPPEIANGYVEHLV R	6,NEIAA_2H(5)[C];	2.0	0.0	0.000	3.41E-02
P31044	GNDISSGTVLSEYVGSGPPK	3,Cation_Na[D];	4.6	0.0	0.000	4.02E-02
Q68FP1	TPSAAYLWVGTGASDAEK	2,Delta_H(5)C(2)[P];	2.0	0.0	0.000	4.74E-02
P09005	ITGTKDLYVSQVVHK	0,Carbamyl[AnyN-term];	4.8	0.0	0.000	2.61E-02
Q63083	LVTLEEFLASTQR	3,Dehydrated[T];	1.0	0.0	0.000	3.41E-02
P22283	LVNCPFEEQTEQLK	4,dichlorination[C];	1.4	0.0	0.000	2.49E-02
Q63621	CDDWGLDTMR	1,Carbamidomethyl[C];	3.8	0.0	0.000	3.04E-02
P19218	CLLGGLGFK	1,Carbamidomethyl[C];	10.2	0.0	0.000	3.93E-02
P12788	HPEYNKDTLDNDIMLIK	0,TMT2plex[AnyN-term];	2.0	0.0	0.000	2.17E-02
Q99PS8	HPPVFGLCR	8,Carbamidomethyl[C];	9.0	0.0	0.000	3.67E-02
Q9JJ19	IVEVNGVCMEGK	8,Carbamidomethyl[C];	6.6	0.0	0.000	1.75E-02
Q9JJ19	IVEVNGVCMEGK	8,Carbamidomethyl[C];9,Oxi dation[M];	4.8	0.0	0.000	3.05E-02
P20059	GECQSEGVLFFQGNR	0,Acetyl_2H(3)[AnyN-term];	9.6	0.0	0.000	4.59E-02
P20059	YYCFQGNK	3,Carbamidomethyl[C];	11.2	0.0	0.000	4.64E-02
P97574	MIAEVQEDCYSK	9,Carbamidomethyl[C];	9.0	0.0	0.000	4.59E-02
P07314	DIQEAGGIMTVEDLNNYR	0,Acetyl_2H(3)[AnyN-term];	3.2	0.0	0.000	4.01E-02
P08592	EVCSEQAETGPCR	3,Carbamidomethyl[C];12,C arbamidomethyl[C];	18.0	0.0	0.000	2.25E-02
P08592	STNLHDYGMLLPCGIDK	13,Carbamidomethyl[C];	7.0	0.0	0.000	1.92E-02
O70535	EIICSWNPGR	4,Carbamidomethyl[C];	6.4	0.0	0.000	3.88E-02
P14562	YSGTCGAQLVTLK	5,Carbamidomethyl[C];	4.0	0.0	0.000	4.74E-02

P14630	TDLFSISCPGGIMLK	8,Carbamidomethyl[C];	5.2	0.0	0.000	1.69E-02
P80067	AISYCHETMTGWVHDVLGR	5,Carbamidomethyl[C];	3.4	0.0	0.000	2.99E-02
Q5FVR0	DEMVPTCWGR	7,Carbamidomethyl[C];	9.6	0.0	0.000	3.55E-02
P02761	VFMQHIDVLENSLGFK	4,Gln->Tyr[Q];	9.0	0.2	0.022	3.28E-02
P82450	QCAVYHTSSVLPAPPFTAR	2,Carbamidomethyl[C];	8.8	0.2	0.023	1.87E-02
P02761	NLDVAKLNGDWFSIVVASNK	6,Xlink_DTSSP[174][K];	16.0	0.4	0.025	4.53E-02
P00787	HCGIESEIVAGIPR	2,Cytopiloyne[C];	8.0	0.2	0.025	2.47E-02
P02761	GETFQLMVLYGR	0,Ethylphosphate[AnyN-term];	23.0	0.6	0.026	4.56E-02
P83121	HICQTYPDEICAWVVVTTR	3,NEM_2H(5)[C];	118.4	3.2	0.027	4.91E-02
P08426	IIRHPSYNANTFDNDIMLIK	7,Tyr->Ala[Y];	6.6	0.2	0.030	1.83E-02
P10960	EVVDSYLPVILDMIK	13,Oxidation[M];	5.2	0.2	0.038	2.04E-02
P47853	VVQCSDLGLK	4,Carbamidomethyl[C];	13.2	0.6	0.045	4.47E-02
P02770	AMCTSFQENPTSFLGHYLHEVAR	3,Carbamidomethyl[C];	4.2	0.2	0.048	3.74E-02
P83121	ICQTYPDEICAWVVVTTR	2,GG[C](Dicarbamidomethyl[C]);10,Carbamidomethyl[C];	6.4	0.4	0.063	2.31E-02
P81827	ICQTYPDEICAWVVVTTR	2,GG[C](Dicarbamidomethyl[C]);10,Carbamidomethyl[C];	6.4	0.4	0.063	2.31E-02
P0DP29	QLTEEQIAEFK	3,PhosphoHex[T];	6.0	0.4	0.067	3.29E-02
P0DP30	QLTEEQIAEFK	3,PhosphoHex[T];	6.0	0.4	0.067	3.29E-02
P0DP31	QLTEEQIAEFK	3,PhosphoHex[T];	6.0	0.4	0.067	3.29E-02
Q5U206	QLTEEQIAEFK	3,PhosphoHex[T];	6.0	0.4	0.067	3.29E-02
P15083	SVSCDQSSQIVSMTLNPVK	0,Unknown_250[AnyN-term];	5.6	0.4	0.071	3.87E-02
P27590	DWMSIVTPAR	3,Carbamidomethyl[M];	11.0	0.8	0.073	2.56E-02
P02761	VFMQHIDVLENSLGFK	2,Phe->Trp[F];	20.4	1.6	0.078	2.45E-02

P01048	DGAETLYSFK	1,Cation_Li[D];	5.0	0.4	0.080	1.69E-02
P08932	DGAETLYSFK	1,Cation_Li[D];	5.0	0.4	0.080	1.69E-02
P02761	EKIEENGSMRVFMQHIDVLENSLGFK	0,GIST-Quat[AnyN-term];	2.4	0.2	0.083	4.02E-02
P83121	PDEICAWVVVTTR	5,Cys->Oxoalanine[C];	2.4	0.2	0.083	2.95E-02
P81828	PDEICAWVVVTTR	5,Cys->Oxoalanine[C];	2.4	0.2	0.083	2.95E-02
P81827	PDEICAWVVVTTR	5,Cys->Oxoalanine[C];	2.4	0.2	0.083	2.95E-02
P02780	LVKPYVQDHFTEK	0,Carbamyl[AnyN-term];	13.6	1.2	0.088	4.05E-02
P02761	EENGSMRVFMQHIDVLENSLGFK	8,Val->Asn[V];	2.2	0.2	0.091	4.74E-02
Q9JHY1	VYSPQTAVQVPENDSVK	0,Phenylisocyanate_2H(5)[AnyN-term];	8.2	0.8	0.098	3.11E-02
P02761	LCEAHGITR	2,Cysteinyl[C];	2.0	0.2	0.100	3.67E-02
P24090	ELACDDPETEHVALIAVDYLNK	4,Carbamidomethyl[C];	12.8	1.4	0.109	2.00E-02
Q68FP1	AAYLWVGTGASDAEK	0,LG-anhydrolactam[AnyN-term];	3.6	0.4	0.111	4.01E-02
P27590	CPHTEDTTIQVTENGESSQAR	2,Pro->Pyrrolidinone[P];	44.8	5.8	0.129	2.94E-02
P07632	ASGEPVVVSGQITGLTEGEHGFHVHQYGDNTQGCTTAGPHFNPH	34,Carbamidomethyl[C];	4.6	0.6	0.130	2.47E-02
P83121	CQTYPDEICAWVVVTTR	9,DTT[C];	110.2	14.6	0.132	2.79E-02
P81828	CQTYPDEICAWVVVTTR	9,DTT[C];	110.2	14.6	0.132	2.79E-02
P81827	CQTYPDEICAWVVVTTR	9,DTT[C];	110.2	14.6	0.132	2.79E-02
P06866	YVMLPVADQEK	3,Oxidation[M];	11.8	1.6	0.136	3.58E-02
P27590	FSIQMFR	5,Oxidation[M];	293.2	40.0	0.136	2.85E-02
P02780	ASGSGCSILDEVIR	0,Amidine[AnyN-term];	1.4	0.2	0.143	3.27E-02
Q9JHB9	ASGSGCSILDEVIR	0,Amidine[AnyN-term];	1.4	0.2	0.143	3.27E-02
P15083	SSVTFECDLGR	7,Carbamidomethyl[C];	52.8	9.4	0.178	3.26E-02

P11232	AFQEALAAAGDK	0,Pyridylacetyl[AnyN-term](Phenylisocyanate[AnyN-term]);	2.2	0.4	0.182	3.67E-02
P02770	TVMGDFAQFVDK	1,Thr->Val[T];	3.2	0.8	0.250	4.18E-02
P27590	CPHTEDTTIQVTENGESSQAR	1,Carbamidomethyl[C];	629.8	162.2	0.258	4.96E-02
O35568	DIDECDIVPDACK	5,Carbamidomethyl[C];12,Carbamidomethyl[C];	10.0	2.6	0.260	2.75E-02
P10252	ILEYFPNGK	7,Deamidated[N];	26.6	7.0	0.263	3.23E-02
P02761	NGETFQLMVLYGR	8,Oxidation[M];	215.8	67.0	0.310	3.03E-02
P02782	NAPPAAVEAK	0,CAF[AnyN-term];	2.4	0.8	0.333	3.49E-02
P01836	KWKIDGSEQRDGVLDSVTDQDSK	3,Xlink_DTSSP[174][K];	1.6	0.6	0.375	3.41E-02
P26644	ITCPPPPIPK	3,Carbamidomethyl[C];	27.8	12.6	0.453	2.26E-02
P36374	KPGNDYSNDLMLLHLK	11,Oxidation[M];	5.0	14.2	2.840	4.97E-02
P00762	TLNNDIMLIK	3,Deamidated[N];	3.2	10.2	3.188	1.07E-02
P00763	TLNNDIMLIK	3,Deamidated[N];	3.2	10.2	3.188	1.07E-02
Q6IMF3	DYQELMNTK	6,Oxidation[M];	8.6	28.0	3.256	4.41E-02
Q63041	VEPGMAPVAK	5,Oxidation[M];	2.2	8.4	3.818	4.23E-02
P27590	CPHTEDTTIQVTENGESSQAR	1,Carbamidomethyl[C];14,Deamidated[N];	1.0	4.8	4.800	4.50E-02
P00762	TLNNDIMLIK	3,Deamidated[N];7,Oxidation[M];	5.2	25.0	4.808	8.11E-04
P00763	TLNNDIMLIK	3,Deamidated[N];7,Oxidation[M];	5.2	25.0	4.808	8.11E-04
P42854	SSGNSGQNVWIGLHDPTLGQEPNR	4,Deamidated[N];8,Deamidated[N];	1.0	5.4	5.400	2.91E-03
P02770	TCVADENAENCDK	2,CarbamidomethylDTT[C];11,Carbamidomethyl[C];	1.6	11.4	7.125	4.09E-02
P22282	LDNCPFEEQTEQLKR	4,CarbamidomethylDTT[C];	2.0	14.8	7.400	2.13E-02

P02770	APQVSTPTLVEAAR	8,Formyl[T](Thr->Glu[T]);	1.6	12.2	7.625	4.08E-02
P02761	LCEAHGITR	8,Sulfo[T];	1.4	10.8	7.714	1.63E-02
P22282	EICYFVVYPDYIEQNIHAVR	0,Amidine[AnyN-term];	0.2	1.8	9.000	3.49E-02
P22282	LDNCPFEEQTEQLKR	4,Carboxymethyl_13C(2)[C];	0.8	7.8	9.750	4.83E-02
Q01177	TAVTAAGTPCQEWAAQEPHSHR	7,Gly->Glu[G];	0.2	2.0	10.000	3.67E-02
P02770	YMCENQATISSK	2,Oxidation[M];3,Carbamidomethyl[C];5,Deamidated[N];	0.2	2.2	11.000	4.74E-02
P81827	CESLDSTGLCR	1,Carbamidomethyl[C];10,CarbamidomethylDTT[C];	4.2	48.6	11.571	3.22E-02
P81827	CESLDSTGLCR	1,CarbamidomethylDTT[C];10,Carbamidomethyl[C];	2.6	41.0	15.769	3.33E-02
Q6P7A9	AVPTQCDVTPNSR	6,Carbamidomethyl[C];	0.6	9.8	16.333	3.55E-03
Q01177	TAAGTPCQEWAAQEPHSHR	7,BADGE[C];	0.8	16.0	20.000	5.84E-03
P02770	TVMGDFAQFVDK	3,Met->Lys[M];	0.2	5.8	29.000	2.64E-02

4 结论

大鼠摄入食用油一周后尿液蛋白质组发生了明显的变化，且不同的食用油种类对大鼠尿蛋白质组的影响存在显著差异，其对大鼠机体的影响是综合全面的。与尿液蛋白质组本身相比，蛋白质组的翻译后修饰变化较小，表明短期内摄入食用油对蛋白质翻译后修饰的影响较为有限。

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